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 Ferrara, Napoleone  
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 Gao, Wei-Qiang  
 Goddard, Audrey  
 Godowski, Paul J.  
 Grimaldi, Christopher J.  
 Gurney, Austin L.  
 Hillan, Kenneth J.  
 Pan, James  
 Paoni, Nicholas F.  
 Roy, Margaret Ann  
 Smith, Victoria  
 Stewart, Timothy A.  
 Tumas, Daniel  
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 Williams, P. Mickey  
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 gaggtcccg gttcctaacgg actgcaagat ggaggaaggc gggaacctag 150  
 gaggcctgat taagatggtc catctactgg tcttgtcagg tgcttggggc 200  
 atgcaaattgt ggggtgacctt cgtctcaggc ttctgtcttt tccgaagcct 250  
 tccccgacat accttcggac tagtgcagag caaactcttc cccttctact 300  
 tccacatctc catgggctgt gccttcatca acctctgcat cttggcttca 350  
 cagcatgctt ggggtcagct cacattctgg gaggccagcc agctttacct 400  
 gctgttctcg agccttacgc tggccactgt caacgcccgc tggctggaac 450

cccgcaccac agctgccatg tgggccctgc aaaccgtgga gaaggagcga 500  
 ggcctgggtg gggaggtacc aggcagccac caggggtcccg atccctaccg 550  
 ccagctgcga gagaaggacc ccaagtacag tgctctccgc cagaatttct 600  
 tccgctacca tgggctgtcc tctctttgca atctgggctg cgtcctgagc 650  
 aatgggctct gtctcgctgg ccttgccctg gaaataagga gcctctagca 700  
 tgggccctgc atgctaataa atgcttcttc agaaatgaaa aaaaaaaaaa 750  
 aaaaaa 756

<210> 8  
 <211> 189  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> sig\_peptide  
 <222> 1-24  
 <223> Signal Peptide

<220>  
 <221> misc\_feature  
 <222> 4-10, 5-11, 47-53, 170-176, 176-182  
 <223> N-Myristoylation Site.

<220>  
 <221> misc\_feature  
 <222> 44-85  
 <223> G-protein Coupled Receptors Proteins.

<220>  
 <221> misc\_feature  
 <222> 54-65  
 <223> Prokaryotic Membrane Lipoprotein Lipid Attachment Site.

<220>  
 <221> misc\_feature  
 <222> 82-86  
 <223> Casein Kinase II Phosphorylation Site.

<220>  
 <221> TRANSMEM  
 <222> 86-103, 60-75  
 <223> Transmembrane Domain

<220>  
 <221> misc\_feature  
 <222> 144-151  
 <223> Tyrosine Kinase Phosphorylation Site.

<400> 8  
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 1 5 10 15

Leu Leu Val Leu Ser Gly Ala Trp Gly Met Gln Met Trp Val Thr  
20 25 30

Phe Val Ser Gly Phe Leu Leu Phe Arg Ser Leu Pro Arg His Thr  
35 40 45

Phe Gly Leu Val Gln Ser Lys Leu Phe Pro Phe Tyr Phe His Ile  
50 55 60

Ser Met Gly Cys Ala Phe Ile Asn Leu Cys Ile Leu Ala Ser Gln  
65 70 75

His Ala Trp Ala Gln Leu Thr Phe Trp Glu Ala Ser Gln Leu Tyr  
80 85 90

Leu Leu Phe Leu Ser Leu Thr Leu Ala Thr Val Asn Ala Arg Trp  
95 100 105

Leu Glu Pro Arg Thr Thr Ala Ala Met Trp Ala Leu Gln Thr Val  
110 115 120

Glu Lys Glu Arg Gly Leu Gly Gly Glu Val Pro Gly Ser His Gln  
125 130 135

Gly Pro Asp Pro Tyr Arg Gln Leu Arg Glu Lys Asp Pro Lys Tyr  
140 145 150

Ser Ala Leu Arg Gln Asn Phe Phe Arg Tyr His Gly Leu Ser Ser  
155 160 165

Leu Cys Asn Leu Gly Cys Val Leu Ser Asn Gly Leu Cys Leu Ala  
170 175 180

Gly Leu Ala Leu Glu Ile Arg Ser Leu  
185

<210> 9  
<211> 1508  
<212> DNA  
<213> Homo sapiens

<400> 9  
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ggacaccatc ttcttgtatt atacaagaaa ggagtgtacc tatcacacac 100  
agggggaaaa atgctctttt ggggtgctagg cctcctaata ctctgtgggt 150  
ttctgtggac tcgtaaagga aaactaaaga ttgaagacat cactgataag 200  
tacattttta tcaactggatg tgactcgggc tttggaaact tggcagccag 250  
aacttttgat aaaaagggat ttcattgtaat cgctgcctgt ctgactgaat 300  
caggatcaac agctttaaag gcagaaacct cagagagact tcgtactgtg 350  
cttctggatg tgaccgaccc agagaatgtc aagaggactg cccagtgggt 400

gaagaaccaa gttggggaga aaggtctctg gggctctgac aataatgctg 450  
 gtgttcccgg cgtgctggct cccactgact ggctgacact agaggactac 500  
 agagaaccta ttgaagttaa cctgtttgga ctcacagtg tgacactaaa 550  
 tatgcttcct ttggtcaaga aagctcaagg gagagttatt aatgtctcca 600  
 gtgttggagg tcgccttgca atcgttggag ggggctatac tccatccaaa 650  
 tatgcagtgg aaggtttcaa tgacagctta agacgggaca tgaaagcttt 700  
 tgggtgtgcac gtctcatgca ttgaaccagg attgttcaaa acaaacttgg 750  
 cagatccagt aaaggttaatt gaaaaaaaaac tcgccatttg ggagcagctg 800  
 tctccagaca tcaaacaaca atatggagaa ggttacattg aaaaaagtct 850  
 agacaaactg aaaggcaata aatcctatgt gaacatggac ctctctccgg 900  
 tggtagagtg catggaccac gctctaacaa gtctcttccc taagactcat 950  
 tatgccgctg gaaaagatgc caaaattttc tggatacctc tgtctcacat 1000  
 gccagcagct ttgcaagact ttttattggt gaaacagaaa gcagagctgg 1050  
 ctaatcccaa ggcagtgtga ctcagctaac cacaaatgtc tcctccaggc 1100  
 tatgaaattg gccgatttca agaacacatc tccttttcaa cccattcct 1150  
 tatctgctcc aacctggact catttagatc gtgcttattt ggattgcaaa 1200  
 agggagtccc accatcgctg gtggtatccc agggtccttg ctcaagtttt 1250  
 ctttgaagag gagggctgga atggtacatc acataggcaa gtcctgccct 1300  
 gtatttaggc tttgcctgct tgggtgtgat taagggaat tgaaagactt 1350  
 gccattcaa aatgatcttt accgtggcct gcccattgct tatggtcccc 1400  
 agcatttaca gtaacttggt aatgttaagt atcatctctt atctaaatat 1450  
 taaaagataa gtcaacccaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1500  
 aaaaaaaaa 1508

<210> 10  
 <211> 319  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> sig\_peptide  
 <222> 1-17  
 <223> Signal Peptide

<220>  
 <221> misc\_feature

<222> 36-47, 108-113, 166-171,198-203, 207-212

<223> N-myristoylation Sites.

<220>

<221> misc\_feature

<222> 39-42

<223> Glycosaminoglycan Attachment Site.

<220>

<221> TRANSMEM

<222> 136-152

<223> Transmembrane Domain

<220>

<221> misc\_feature

<222> 161-163, 187-190 and 253-256

<223> N-glycosylation Sites.

<400> 10

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Trp	Thr	Arg	Lys	Gly	Lys	Leu	Lys	Ile	Glu	Asp	Ile	Thr	Asp	Lys
				20					25					30
Tyr	Ile	Phe	Ile	Thr	Gly	Cys	Asp	Ser	Gly	Phe	Gly	Asn	Leu	Ala
				35					40					45
Ala	Arg	Thr	Phe	Asp	Lys	Lys	Gly	Phe	His	Val	Ile	Ala	Ala	Cys
				50					55					60
Leu	Thr	Glu	Ser	Gly	Ser	Thr	Ala	Leu	Lys	Ala	Glu	Thr	Ser	Glu
				65					70					75
Arg	Leu	Arg	Thr	Val	Leu	Leu	Asp	Val	Thr	Asp	Pro	Glu	Asn	Val
				80					85					90
Lys	Arg	Thr	Ala	Gln	Trp	Val	Lys	Asn	Gln	Val	Gly	Glu	Lys	Gly
				95					100					105
Leu	Trp	Gly	Leu	Ile	Asn	Asn	Ala	Gly	Val	Pro	Gly	Val	Leu	Ala
				110					115					120
Pro	Thr	Asp	Trp	Leu	Thr	Leu	Glu	Asp	Tyr	Arg	Glu	Pro	Ile	Glu
				125					130					135
Val	Asn	Leu	Phe	Gly	Leu	Ile	Ser	Val	Thr	Leu	Asn	Met	Leu	Pro
				140					145					150
Leu	Val	Lys	Lys	Ala	Gln	Gly	Arg	Val	Ile	Asn	Val	Ser	Ser	Val
				155					160					165
Gly	Gly	Arg	Leu	Ala	Ile	Val	Gly	Gly	Gly	Tyr	Thr	Pro	Ser	Lys
				170					175					180
Tyr	Ala	Val	Glu	Gly	Phe	Asn	Asp	Ser	Leu	Arg	Arg	Asp	Met	Lys
				185					190					195



Ala	Phe	Gly	Val	His	Val	Ser	Cys	Ile	Glu	Pro	Gly	Leu	Phe	Lys
				200					205					210
Thr	Asn	Leu	Ala	Asp	Pro	Val	Lys	Val	Ile	Glu	Lys	Lys	Leu	Ala
				215					220					225
Ile	Trp	Glu	Gln	Leu	Ser	Pro	Asp	Ile	Lys	Gln	Gln	Tyr	Gly	Glu
				230					235					240
Gly	Tyr	Ile	Glu	Lys	Ser	Leu	Asp	Lys	Leu	Lys	Gly	Asn	Lys	Ser
				245					250					255
Tyr	Val	Asn	Met	Asp	Leu	Ser	Pro	Val	Val	Glu	Cys	Met	Asp	His
				260					265					270
Ala	Leu	Thr	Ser	Leu	Phe	Pro	Lys	Thr	His	Tyr	Ala	Ala	Gly	Lys
				275					280					285
Asp	Ala	Lys	Ile	Phe	Trp	Ile	Pro	Leu	Ser	His	Met	Pro	Ala	Ala
				290					295					300
Leu	Gln	Asp	Phe	Leu	Leu	Leu	Lys	Gln	Lys	Ala	Glu	Leu	Ala	Asn
				305					310					315
Pro	Lys	Ala	Val											

<210> 11  
 <211> 2720  
 <212> DNA  
 <213> Homo sapiens

<400> 11  
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 gccccttggg ccgtcgccac cactgtagtc atgtaccac cgccgccgcc 150  
 gccgcctcat cgggacttca tctcggtgac gctgagcttt ggcgagagct 200  
 atgacaacag caagagttgg cggcggcgct cgtgctggag gaaatggaag 250  
 caactgtcga gattgcagcg gaatatgatt ctcttctcc ttgcctttct 300  
 gcttttctgt ggactcctct tctacatcaa cttggctgac cattggaaag 350  
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 ggggttaaacc cagcaaacc acccgcttta ccagtcctc agaaggcgga 450  
 caccgaccct gagaacttac ctgagatttc gtcacagaag acacaaagac 500  
 acatccagcg gggaccacct cacctgcaga ttagaccccc aagccaagac 550  
 ctgaaggatg ggaccagga ggaggccaca aaaaggcaag aagcccctgt 600  
 ggatccccgc ccggaaggag atccgcagag gacagtcac agctggaggg 650

gagcggatgat cgagcctgag cagggcaccg agctcccttc aagaagagca 700  
 gaagtgccca ccaagcctcc cctgccaccg gccaggacac agggcacacc 750  
 agtgcattctg aactatcgcc agaagggcgt gattgacgtc ttcttgcattg 800  
 catggaaagg ataccgcaag tttgcatggg gccatgacga gctgaagcct 850  
 gtgtccagggt ccttcagtga gtgggtttggc ctcggtctca cactgatcga 900  
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 aacctgctca gcctggacgc ctacgtgttc aacaccgaag cccaccctct 2100

gcctatctgg acccctgcct aggggtggatg gctgctggtg tggggacttc 2150  
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 cctcctggcc gccccgcagg gggcttggag ggctggacgg caagtccgtc 2650  
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 ttgatttgct ctaaccgcaa 2720

<210> 12  
 <211> 699  
 <212> PRT  
 <213> Homo sapiens  
 <220>  
 <221> TRANSMEM  
 <222> 21-40 and 84-105  
 <223> Transmembrane Domain (type II)

<400> 12  
 Met Ala Ala Cys Glu Gly Arg Arg Ser Gly Ala Leu Gly Ser Ser  
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 Gln Ser Asp Phe Leu Thr Pro Pro Val Gly Gly Ala Pro Trp Ala  
 20 25 30  
 Val Ala Thr Thr Val Val Met Tyr Pro Pro Pro Pro Pro Pro  
 35 40 45  
 His Arg Asp Phe Ile Ser Val Thr Leu Ser Phe Gly Glu Ser Tyr  
 50 55 60  
 Asp Asn Ser Lys Ser Trp Arg Arg Arg Ser Cys Trp Arg Lys Trp  
 65 70 75  
 Lys Gln Leu Ser Arg Leu Gln Arg Asn Met Ile Leu Phe Leu Leu  
 80 85 90  
 Ala Phe Leu Leu Phe Cys Gly Leu Leu Phe Tyr Ile Asn Leu Ala  
 95 100 105

Asp	His	Trp	Lys	Ala	Leu	Ala	Phe	Arg	Leu	Glu	Glu	Glu	Gln	Lys	
				110					115					120	
Met	Arg	Pro	Glu	Ile	Ala	Gly	Leu	Lys	Pro	Ala	Asn	Pro	Pro	Val	
				125					130					135	
Leu	Pro	Ala	Pro	Gln	Lys	Ala	Asp	Thr	Asp	Pro	Glu	Asn	Leu	Pro	
				140					145					150	
Glu	Ile	Ser	Ser	Gln	Lys	Thr	Gln	Arg	His	Ile	Gln	Arg	Gly	Pro	
				155					160					165	
Pro	His	Leu	Gln	Ile	Arg	Pro	Pro	Ser	Gln	Asp	Leu	Lys	Asp	Gly	
				170					175					180	
Thr	Gln	Glu	Glu	Ala	Thr	Lys	Arg	Gln	Glu	Ala	Pro	Val	Asp	Pro	
				185					190					195	
Arg	Pro	Glu	Gly	Asp	Pro	Gln	Arg	Thr	Val	Ile	Ser	Trp	Arg	Gly	
				200					205					210	
Ala	Val	Ile	Glu	Pro	Glu	Gln	Gly	Thr	Glu	Leu	Pro	Ser	Arg	Arg	
				215					220					225	
Ala	Glu	Val	Pro	Thr	Lys	Pro	Pro	Leu	Pro	Pro	Ala	Arg	Thr	Gln	
				230					235					240	
Gly	Thr	Pro	Val	His	Leu	Asn	Tyr	Arg	Gln	Lys	Gly	Val	Ile	Asp	
				245					250					255	
Val	Phe	Leu	His	Ala	Trp	Lys	Gly	Tyr	Arg	Lys	Phe	Ala	Trp	Gly	
				260					265					270	
His	Asp	Glu	Leu	Lys	Pro	Val	Ser	Arg	Ser	Phe	Ser	Glu	Trp	Phe	
				275					280					285	
Gly	Leu	Gly	Leu	Thr	Leu	Ile	Asp	Ala	Leu	Asp	Thr	Met	Trp	Ile	
				290					295					300	
Leu	Gly	Leu	Arg	Lys	Glu	Phe	Glu	Glu	Ala	Arg	Lys	Trp	Val	Ser	
				305					310					315	
Lys	Lys	Leu	His	Phe	Glu	Lys	Asp	Val	Asp	Val	Asn	Leu	Phe	Glu	
				320					325					330	
Ser	Thr	Ile	Arg	Ile	Leu	Gly	Gly	Leu	Leu	Ser	Ala	Tyr	His	Leu	
				335					340					345	
Ser	Gly	Asp	Ser	Leu	Phe	Leu	Arg	Lys	Ala	Glu	Asp	Phe	Gly	Asn	
				350					355					360	
Arg	Leu	Met	Pro	Ala	Phe	Arg	Thr	Pro	Ser	Lys	Ile	Pro	Tyr	Ser	
				365					370					375	
Asp	Val	Asn	Ile	Gly	Thr	Gly	Val	Ala	His	Pro	Pro	Arg	Trp	Thr	
				380					385					390	
Ser	Asp	Ser	Thr	Val	Ala	Glu	Val	Thr	Ser	Ile	Gln	Leu	Glu	Phe	

	395	400	405
Arg Glu Leu Ser	Arg Leu Thr Gly Asp Lys Lys Phe Gln Glu Ala		
	410	415	420
Val Glu Lys Val	Thr Gln His Ile His Gly Leu Ser Gly Lys Lys		
	425	430	435
Asp Gly Leu Val	Pro Met Phe Ile Asn Thr His Ser Gly Leu Phe		
	440	445	450
Thr His Leu Gly	Val Phe Thr Leu Gly Ala Arg Ala Asp Ser Tyr		
	455	460	465
Tyr Glu Tyr Leu	Leu Lys Gln Trp Ile Gln Gly Gly Lys Gln Glu		
	470	475	480
Thr Gln Leu Leu	Glu Asp Tyr Val Glu Ala Ile Glu Gly Val Arg		
	485	490	495
Thr His Leu Leu	Arg His Ser Glu Pro Ser Lys Leu Thr Phe Val		
	500	505	510
Gly Glu Leu Ala	His Gly Arg Phe Ser Ala Lys Met Asp His Leu		
	515	520	525
Val Cys Phe Leu	Pro Gly Thr Leu Ala Leu Gly Val Tyr His Gly		
	530	535	540
Leu Pro Ala Ser	His Met Glu Leu Ala Gln Glu Leu Met Glu Thr		
	545	550	555
Cys Tyr Gln Met	Asn Arg Gln Met Glu Thr Gly Leu Ser Pro Glu		
	560	565	570
Ile Val His Phe	Asn Leu Tyr Pro Gln Pro Gly Arg Arg Asp Val		
	575	580	585
Glu Val Lys Pro	Ala Asp Arg His Asn Leu Leu Arg Pro Glu Thr		
	590	595	600
Val Glu Ser Leu	Phe Tyr Leu Tyr Arg Val Thr Gly Asp Arg Lys		
	605	610	615
Tyr Gln Asp Trp	Gly Trp Glu Ile Leu Gln Ser Phe Ser Arg Phe		
	620	625	630
Thr Arg Val Pro	Ser Gly Gly Tyr Ser Ser Ile Asn Asn Val Gln		
	635	640	645
Asp Pro Gln Lys	Pro Glu Pro Arg Asp Lys Met Glu Ser Phe Phe		
	650	655	660
Leu Gly Glu Thr	Leu Lys Tyr Leu Phe Leu Leu Phe Ser Asp Asp		
	665	670	675
Pro Asn Leu Leu	Ser Leu Asp Ala Tyr Val Phe Asn Thr Glu Ala		
	680	685	690

His Pro Leu Pro Ile Trp Thr Pro Ala  
695

<210> 13  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 13  
cgccagaagg gcgtgattga cgtc 24

<210> 14  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 14  
ccatccttct tcccagacag gccg 24

<210> 15  
<211> 44  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-44  
<223> Synthetic construct.

<400> 15  
gaagcctgtg tccaggtoct tcaagtgagt gtttggcctc ggtc 44

<210> 16  
<211> 1524  
<212> DNA  
<213> Homo sapiens

<400> 16  
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ccctcggaag tgttccgtct tccacctgtt cgtggcctgc ctctcgtctg 200  
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cgggcagtca ggggacaagg gcaggagacc tcgggccctc cccgtgcctg 300  
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 cccaccgcct ggcagtgtctg gtgcccttcc gcgaacgctt cgaggagctc 400  
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 cagcactacc ggctgtgcaa tgggatgtcc aaccgcttct ggggtgtggg 750  
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 ttttccgccc ctcggaatc acaactgggt acaagacatt tcgccacctg 850  
 catgaccag cctggcgga gagggaccag aagcgcatcg cagctcaaaa 900  
 acaggagcag ttcaagggtg acaggaggagg aggcctgaac actgtgaagt 950  
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 ttgctcaggc tcaggacaag gcctcaggtc gtgggcccag ctctgacagg 1150  
 atgtggagtg gccaggacca agacagcaag ctacgcaatt gcagccacc 1200  
 ggccgccaag gcaggcttgg gctgggcccag gacacgtggg gtgcctggga 1250  
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 cgggaccccc cctgccttcc tgcctaccct actctgacct ccttcacgtg 1350  
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 cctactctga cctccttcac gtgcccaggc ctgtgggtag tggggagggc 1450  
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 <211> 327  
 <212> PRT  
 <213> Homo sapiens  
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<212> DNA  
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<220>  
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<213> Homo sapiens

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gactggtcgg tgcccagaaa gtctcttctg ccactgacgc ccccatcagg 150  
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<211> 73  
<212> PRT  
<213> Homo sapiens

<220>  
<221> sig\_peptide  
<222> 1-15  
<223> Signal peptide.

<220>  
<221> misc\_feature  
<222> 3-18

<223> Growth factor and cytokines receptors family.

<400> 22

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Ala Thr Asp Ala Pro Ile Arg Asp Trp Ala Phe Phe Pro Pro Ser  
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<212> DNA

<213> Homo sapiens

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Asn	Lys	Ile	Ser	Glu	Leu	Lys	Asn	Gly	Ser	Phe	Ser	Gly	Leu	Ser	
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Asp	Pro	Gly	Ala	Phe	Trp	Gly	Leu	Ser	Ser	Leu	Lys	Arg	Leu	Asp	
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Gly	Leu	Thr	Asn	Leu	Val	Arg	Leu	Asn	Leu	Ser	Gly	Asn	Leu	Phe	
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Ser	Leu	Glu	Phe	Gln	Thr	Glu	Tyr	Leu	Leu	Cys	Asp	Cys	Asn	Ile	
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Leu	Trp	Met	His	Arg	Trp	Val	Lys	Glu	Lys	Asn	Ile	Thr	Val	Arg	
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Glu	Gly	Asp	Ser	Leu	Pro	Phe	Gln	Cys	Met	Ala	Ser	Tyr	Ile	Asp	
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Gln	Asp	Met	Gln	Val	Leu	Trp	Tyr	Gln	Asp	Gly	Arg	Ile	Val	Glu	
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Thr	Asp	Glu	Ser	Gln	Gly	Ile	Phe	Val	Glu	Lys	Asn	Met	Ile	His	
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Asn	Cys	Ser	Leu	Ile	Ala	Ser	Ala	Leu	Thr	Ile	Ser	Asn	Ile	Gln	
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Ala	Gly	Ser	Thr	Gly	Asn	Trp	Gly	Cys	His	Val	Gln	Thr	Lys	Arg	
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Gly	Asn	Asn	Thr	Arg	Thr	Val	Asp	Ile	Val	Val	Leu	Glu	Ser	Ser	
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Phe	Arg	Trp	Pro	Arg	Thr	Leu	Ala	Gly	Ile	Thr	Ala	Tyr	Leu	Gln	
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Trp	Ala	Asp	Asp	Asp	Tyr	Ser	Arg	Cys	Gln	Tyr	Ala	Asn	Asp	Val					
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Thr	Arg	Val	Leu	Tyr	Met	Phe	Asn	Gln	Met	Pro	Leu	Asn	Leu	Thr					
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Cys	Ser	Arg	Ile	Val	Gln	Cys	Leu	Gln	Arg	Ile	Ala	Thr	Tyr	Arg					
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Leu	Ser	Asp	Tyr	Gly	Arg	Arg	Asp	Pro	Glu	Gly	Asn	Leu	Asp	Lys					
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Gln	Leu	Ser	Phe	Lys	Cys	Asn	Val	Ser	Asn	Thr	Phe	Ser	Ser	Leu					
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- <211> 24
- <212> DNA
- <213> Artificial
- <220>
- <221> Artificial Sequence
- <222> 1-24





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 35 40 45  
 Ile Arg Lys Lys Glu Asn Ile Arg Leu Leu Gly Glu Gln Ile Ile  
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<211> 322

<212> PRT

<213> Homo sapiens

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Ser	Thr	Cys	Val	Ala	Phe	Ser	Leu	Val	Ala	Ser	Val	Gly	Ala	Trp	
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Thr	Gly	Ser	Met	Gly	Asn	Trp	Ser	Met	Phe	Thr	Trp	Cys	Phe	Cys	
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Phe	Ser	Val	Thr	Leu	Ile	Ile	Leu	Ile	Val	Glu	Leu	Cys	Gly	Leu	
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Gln	Ala	Arg	Phe	Pro	Leu	Ser	Trp	Arg	Asn	Phe	Pro	Ile	Thr	Phe	
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Ala	Cys	Tyr	Ala	Ala	Leu	Phe	Cys	Leu	Ser	Ala	Ser	Ile	Ile	Tyr	
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Pro	Thr	Thr	Tyr	Val	Gln	Phe	Leu	Ser	His	Gly	Arg	Ser	Arg	Asp	
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His	Ala	Ile	Ala	Ala	Thr	Phe	Phe	Ser	Cys	Ile	Ala	Cys	Val	Ala	
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Tyr	Ala	Thr	Glu	Val	Ala	Trp	Thr	Arg	Ala	Arg	Pro	Gly	Glu	Ile	
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Thr	Phe	Val	Ala	Cys	Ile	Ile	Phe	Ala	Phe	Ile	Ser	Asp	Pro	Asn	
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Val Leu Trp Pro Leu Tyr Gln Phe Asp Glu Lys Tyr Gly Gly Gln  
260 265 270  
Pro Arg Arg Ser Arg Asp Val Ser Cys Ser Arg Ser His Ala Tyr  
275 280 285  
Tyr Val Cys Ala Trp Asp Arg Arg Leu Ala Val Ala Ile Leu Thr  
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<212> DNA  
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<210> 33

<211> 335

<212> PRT

<213> Homo sapiens

<400> 33

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				20					25					30
Ser	Leu	Ala	Gln	Val	Asn	Leu	Ser	Pro	Phe	Ser	His	Pro	Lys	Val
				35					40					45
His	Met	Asp	Pro	Asn	Tyr	Cys	His	Pro	Ser	Thr	Ser	Leu	His	Leu
				50					55					60
Cys	Ser	Leu	Ala	Trp	Ser	Phe	Thr	Arg	Leu	Leu	His	Pro	Pro	Leu
				65					70					75
Ser	Pro	Gly	Ile	Ser	Gln	Val	Val	Lys	Asp	His	Val	Thr	Lys	Pro
				80					85					90
Thr	Ala	Met	Ala	Gln	Gly	Arg	Val	Ala	His	Leu	Ile	Glu	Trp	Lys
				95					100					105
Gly	Trp	Ser	Lys	Pro	Ser	Asp	Ser	Pro	Ala	Ala	Leu	Glu	Ser	Ala
				110					115					120
Phe	Ser	Ser	Tyr	Ser	Asp	Leu	Ser	Glu	Gly	Glu	Gln	Glu	Ala	Arg
				125					130					135
Phe	Ala	Ala	Gly	Val	Ala	Glu	Gln	Phe	Ala	Ile	Ala	Glu	Ala	Lys
				140					145					150
Leu	Arg	Ala	Trp	Ser	Ser	Val	Asp	Gly	Glu	Asp	Ser	Thr	Asp	Asp
				155					160					165
Ser	Tyr	Asp	Glu	Asp	Phe	Ala	Gly	Gly	Met	Asp	Thr	Asp	Met	Ala
				170					175					180
Gly	Gln	Leu	Pro	Leu	Gly	Pro	His	Leu	Gln	Asp	Leu	Phe	Thr	Gly
				185					190					195
His	Arg	Phe	Ser	Arg	Pro	Val	Arg	Gln	Gly	Ser	Val	Glu	Pro	Glu
				200					205					210
Ser	Asp	Cys	Ser	Gln	Thr	Val	Ser	Pro	Asp	Thr	Leu	Cys	Ser	Ser
				215					220					225
Leu	Cys	Ser	Leu	Glu	Asp	Gly	Leu	Leu	Gly	Ser	Pro	Ala	Arg	Leu
				230					235					240

Ala Ser Gln Leu Leu Gly Asp Glu Leu Leu Leu Ala Lys Leu Pro  
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Pro Ser Arg Glu Ser Ala Phe Arg Ser Leu Gly Pro Leu Glu Ala  
260 265 270

Gln Asp Ser Leu Tyr Asn Ser Pro Leu Thr Glu Ser Cys Leu Ser  
275 280 285

Pro Ala Glu Glu Glu Pro Ala Pro Cys Lys Asp Cys Gln Pro Leu  
290 295 300

Cys Pro Pro Leu Thr Gly Ser Trp Glu Arg Gln Arg Gln Ala Ser  
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<210> 34  
<211> 25  
<212> DNA  
<213> Artificial

<220>  
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<222> 1-25  
<223> Synthetic construct

<400> 34  
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<210> 35  
<211> 50  
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<220>  
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<222> 1-50  
<223> Synthetic construct.

<400> 35  
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<210> 36  
<211> 25  
<212> DNA  
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<220>  
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<223> Synthetic construct.

<400> 36



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1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

<213> Artificial

<223> Synthetic construct.

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<213> Artificial

<223> Synthetic construct.

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<213> Artificial

<223> Synthetic construct.

ctgctgcaaa qcgagcctct tq 22

<213> Homo sapiens

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<210> 41  
<211> 334  
<212> PRT  
<213> Homo sapiens

<400> 41  
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Thr Thr Gln Asn Ile Ala Glu Val Phe Lys Thr Met Glu Asn Lys  
35 40 45  
Pro Ile Ser Leu Glu Ser Glu Ala Asn Leu Asn Ser Asp Lys Glu  
50 55 60  
Asn Ile Thr Thr Ser Asn Leu Lys Ala Ser His Ser Pro Pro Leu  
65 70 75  
Asn Leu Pro Asn Asn Ser His Gly Ile Thr Asp Phe Ser Ser Asn  
80 85 90  
Ser Ser Ala Glu His Ser Leu Gly Ser Leu Lys Pro Thr Ser Thr  
95 100 105  
Ile Ser Thr Ser Pro Pro Leu Ile His Ser Phe Val Ser Lys Val  
110 115 120  
Pro Trp Asn Ala Pro Ile Ala Asp Glu Asp Leu Leu Pro Ile Ser  
125 130 135  
Ala His Pro Asn Ala Thr Pro Ala Leu Ser Ser Glu Asn Phe Thr  
140 145 150  
Trp Ser Leu Val Asn Asp Thr Val Lys Thr Pro Asp Asn Ser Ser  
155 160 165  
Ile Thr Val Ser Ile Leu Ser Ser Glu Pro Thr Ser Pro Ser Val  
170 175 180  
Thr Pro Leu Ile Val Glu Pro Ser Gly Trp Leu Thr Thr Asn Ser  
185 190 195













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<210> 50

<211> 283

<212> PRT

<213> Homo sapiens

<400> 50

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Leu	Leu	Gly	Ser	Val	Pro	Ala	Thr	Asp	Ala	Arg	Ser	Val	Pro	Leu	
				20					25					30	
Lys	Ala	Thr	Phe	Leu	Glu	Asp	Val	Ala	Gly	Ser	Gly	Glu	Ala	Glu	
				35					40					45	
Gly	Ser	Ser	Ala	Ser	Ser	Pro	Ser	Leu	Pro	Pro	Pro	Trp	Thr	Pro	
				50					55					60	
Ala	Leu	Ser	Pro	Thr	Ser	Met	Gly	Pro	Gln	Pro	Thr	Thr	Leu	Gly	
				65					70					75	
Gly	Pro	Ser	Pro	Pro	Thr	Asn	Phe	Leu	Asp	Gly	Ile	Val	Asp	Phe	
				80					85					90	
Phe	Arg	Gln	Tyr	Val	Met	Leu	Ile	Ala	Val	Val	Gly	Ser	Leu	Ala	
				95					100					105	
Phe	Leu	Leu	Met	Phe	Ile	Val	Cys	Ala	Ala	Val	Ile	Thr	Arg	Gln	
				110					115					120	
Lys	Gln	Lys	Ala	Ser	Ala	Tyr	Tyr	Pro	Ser	Ser	Phe	Pro	Lys	Lys	
				125					130					135	
Lys	Tyr	Val	Asp	Gln	Ser	Asp	Arg	Ala	Gly	Gly	Pro	Arg	Ala	Phe	
				140					145					150	
Ser	Glu	Val	Pro	Asp	Arg	Ala	Pro	Asp	Ser	Arg	Pro	Glu	Glu	Ala	
				155					160					165	



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<210> 52  
 <211> 440  
 <212> PRT  
 <213> Homo sapiens

<400> 52  
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 20 25 30  
 Thr Gly Thr Asn Ile Gly Glu Ala Leu Gly His Gly Leu Gly Asp  
 35 40 45  
 Ala Leu Ser Glu Gly Val Gly Lys Ala Ile Gly Lys Glu Ala Gly

	50		55		60
Gly Ala Ala Gly	Ser Lys Val Ser Glu	Ala Leu Gly Gln Gly Thr			
	65	70			75
Arg Glu Ala Val	Gly Thr Gly Val Arg	Gln Val Pro Gly Phe Gly			
	80	85			90
Ala Ala Asp Ala	Leu Gly Asn Arg Val	Gly Glu Ala Ala His Ala			
	95	100			105
Leu Gly Asn Thr	Gly His Glu Ile Gly	Arg Gln Ala Glu Asp Val			
	110	115			120
Ile Arg His Gly	Ala Asp Ala Val Arg	Gly Ser Trp Gln Gly Val			
	125	130			135
Pro Gly His Ser	Gly Ala Trp Glu Thr	Ser Gly Gly His Gly Ile			
	140	145			150
Phe Gly Ser Gln	Gly Gly Leu Gly Gly	Gln Gly Gln Gly Asn Pro			
	155	160			165
Gly Gly Leu Gly	Thr Pro Trp Val His	Gly Tyr Pro Gly Asn Ser			
	170	175			180
Ala Gly Ser Phe	Gly Met Asn Pro Gln	Gly Ala Pro Trp Gly Gln			
	185	190			195
Gly Gly Asn Gly	Gly Pro Pro Asn Phe	Gly Thr Asn Thr Gln Gly			
	200	205			210
Ala Val Ala Gln	Pro Gly Tyr Gly Ser	Val Arg Ala Ser Asn Gln			
	215	220			225
Asn Glu Gly Cys	Thr Asn Pro Pro Pro	Ser Gly Ser Gly Gly Gly			
	230	235			240
Ser Ser Asn Ser	Gly Gly Gly Ser Gly	Ser Gln Ser Gly Ser Ser			
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Gly Ser Gly Ser	Asn Gly Asp Asn Asn	Asn Gly Ser Ser Ser Gly			
	260	265			270
Gly Ser Ser Ser	Gly Ser Ser Ser Gly	Ser Ser Ser Gly Gly Ser			
	275	280			285
Ser Gly Gly Ser	Ser Gly Gly Ser Ser	Gly Asn Ser Gly Gly Ser			
	290	295			300
Arg Gly Asp Ser	Gly Ser Glu Ser Ser	Trp Gly Ser Ser Thr Gly			
	305	310			315
Ser Ser Ser Gly	Asn His Gly Gly Ser	Gly Gly Gly Asn Gly His			
	320	325			330
Lys Pro Gly Cys	Glu Lys Pro Gly Asn	Glu Ala Arg Gly Ser Gly			
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Glu Ser Gly Ile Gln Gly Phe Arg Gly Gln Gly Val Ser Ser Asn  
350 355 360  
Met Arg Glu Ile Ser Lys Glu Gly Asn Arg Leu Leu Gly Gly Ser  
365 370 375  
Gly Asp Asn Tyr Arg Gly Gln Gly Ser Ser Trp Gly Ser Gly Gly  
380 385 390  
Gly Asp Ala Val Gly Gly Val Asn Thr Val Asn Ser Glu Thr Ser  
395 400 405  
Pro Gly Met Phe Asn Phe Asp Thr Phe Trp Lys Asn Phe Lys Ser  
410 415 420  
Lys Leu Gly Phe Ile Asn Trp Asp Ala Ile Asn Lys Asp Gln Arg  
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Ser Ser Arg Ile Pro  
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<210> 53  
<211> 3580  
<212> DNA  
<213> Homo sapiens

<400> 53  
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<400> 54

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				20					25					30
Glu	Gly	Pro	Ser	Tyr	Ala	Phe	Glu	Val	Asp	Thr	Val	Ala	Pro	Glu
				35					40					45
His	Gly	Leu	Asp	Asn	Ala	Pro	Val	Val	Asp	Gln	Gln	Leu	Leu	Tyr
				50					55					60
Thr	Cys	Cys	Pro	Tyr	Ile	Gly	Glu	Leu	Arg	Lys	Leu	Leu	Ala	Ser
				65					70					75
Trp	Val	Ser	Gly	Ser	Ser	Gly	Arg	Ser	Gly	Gly	Phe	Met	Arg	Lys
				80					85					90
Ile	Thr	Pro	Thr	Thr	Thr	Thr	Ser	Leu	Gly	Ala	Gln	Pro	Ser	Gln
				95					100					105
Thr	Ser	Gln	Gly	Leu	Gln	Ala	Gln	Leu	Ala	Gln	Ala	Phe	Phe	His
				110					115					120
Asn	Gln	Pro	Pro	Ser	Leu	Arg	Arg	Thr	Val	Glu	Phe	Val	Ala	Glu
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				170					175					180
Ile	Leu	Cys	Ser	Gln	Leu	Cys	Pro	His	Gly	Ala	Gln	Ala	Leu	Ala
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35 40 45

Val Gln Lys Pro Gly Gly Thr Val Ile Leu Gly Cys Val Val Glu  
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Pro Pro Arg Met Asn Val Thr Trp Arg Leu Asn Gly Lys Glu Leu  
65 70 75

Asn Gly Ser Asp Asp Ala Leu Gly Val Leu Ile Thr His Gly Thr  
80 85 90

Leu Val Ile Thr Ala Leu Asn Asn His Thr Val Gly Arg Tyr Gln  
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Cys Val Ala Arg Met Pro Ala Gly Ala Val Ala Ser Val Pro Ala  
110 115 120

Thr Val Thr Leu Ala Asn Leu Gln Asp Phe Lys Leu Asp Val Gln  
125 130 135

His Val Ile Glu Val Asp Glu Gly Asn Thr Ala Val Ile Ala Cys  
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His Leu Pro Glu Ser His Pro Lys Ala Gln Val Arg Tyr Ser Val  
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Lys Gln Glu Trp Leu Glu Ala Ser Arg Gly Asn Tyr Leu Ile Met  
170 175 180

Pro Ser Gly Asn Leu Gln Ile Val Asn Ala Ser Gln Glu Asp Glu  
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Gly Met Tyr Lys Cys Ala Ala Tyr Asn Pro Val Thr Gln Glu Val  
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Lys Thr Ser Gly Ser Ser Asp Arg Leu Arg Val Arg Arg Ser Thr  
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Ala Glu Ala Ala Arg Ile Ile Tyr Pro Pro Glu Ala Gln Thr Ile  
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Ile Val Thr Lys Gly Gln Ser Leu Ile Leu Glu Cys Val Ala Ser  
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Gly Ile Pro Pro Pro Arg Val Thr Trp Ala Lys Asp Gly Ser Ser  
260 265 270

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Gln	Leu	Val	Ile	Pro 335	Trp	Gly	Gln	Ser	Ala 340	Lys	Leu	Thr	Cys	Glu 345
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Pro	Arg	Thr	Ser	Lys 485	Thr	Asp	Ser	Tyr	Glu 490	Leu	Val	Trp	Arg	Pro 495
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Lys	His	Arg	Lys	Gln 515	Val	Thr	Asn	Ser	Ser 520	Asp	Asp	Trp	Thr	Ile 525
Ser	Gly	Ile	Pro	Ala 530	Asn	Gln	His	Arg	Leu 535	Thr	Leu	Thr	Arg	Leu 540
Asp	Pro	Gly	Ser	Leu 545	Tyr	Glu	Val	Glu	Met 550	Ala	Ala	Tyr	Asn	Cys 555
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Thr	Ser	Tyr	Lys	Phe	Arg	Val	Arg	Ala	Leu	Asn	Met	Leu	Gly	Glu																														
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Ser	Glu	Pro	Ser	Ala	Pro	Ser	Arg	Pro	Tyr	Val	Val	Ser	Gly	Tyr																														
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Lys	His	Thr	Thr	Asp	Leu	Gly	Phe	Pro	Arg	Ser	Ala	Leu	Pro	Pro	
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Gln	Ala	Ser	Gly	Gln	Pro	Tyr	Leu	Ser	Gly	Ile	Ser	Gly	Arg	Ala	
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Cys	Ala	Asn	Gly	Ile	His	Met	Asn	Arg	Gly	Cys	Pro	Ser	Ala	Ala	
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Val	Gly	Tyr	Pro	Gly	Met	Lys	Pro	Gln	Gln	His	Cys	Pro	Gly	Glu	
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Asp	Asp	Ser	Thr	His	Gln	Leu	Leu	Gln	Pro	His	His	Asp	Cys	Cys	
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Phe	His	Ser	Gly	Pro	Pro	Cys	Cys	Leu	Gly	Leu	Val	Pro	Val	Glu	
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 <213> Artificial

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<212> PRT
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 <222> 196, 386  
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Gln	Pro	Val	Thr	Arg	Ala	Glu	Thr	Thr	Pro	Gly	Ala	Pro	Arg	Ala	
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Leu	Ser	Thr	Leu	Gly	Ser	Pro	Ser	Leu	Phe	Thr	Thr	Pro	Gly	Val	
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Pro	Ser	Ala	Leu	Thr	Thr	Pro	Gly	Leu	Thr	Thr	Pro	Gly	Thr	Pro	
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Lys	Thr	Leu	Asp	Leu	Arg	Gly	Arg	Ala	Gln	Ala	Leu	Met	Arg	Ser	
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Phe	Pro	Leu	Val	Asp	Gly	His	Asn	Asp	Leu	Pro	Gln	Val	Leu	Arg	
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Gln	Arg	Tyr	Lys	Asn	Val	Leu	Gln	Asp	Val	Asn	Leu	Arg	Asn	Phe	
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Gly	Ala	Gln	Phe	Trp	Ser	Ala	Ser	Val	Ser	Cys	Gln	Ser	Gln	Asp	
				140					145					150	
Gln	Thr	Ala	Val	Arg	Leu	Ala	Leu	Glu	Gln	Ile	Asp	Leu	Ile	His	
				155					160					165	
Arg	Met	Cys	Ala	Ser	Tyr	Ser	Glu	Leu	Glu	Leu	Val	Thr	Ser	Ala	
				170					175					180	
Glu	Gly	Leu	Asn	Ser	Ser	Gln	Lys	Leu	Ala	Cys	Leu	Ile	Gly	Val	
				185					190					195	
Xaa	Gly	Gly	His	Ser	Leu	Asp	Ser	Ser	Leu	Ser	Val	Leu	Arg	Ser	
				200					205					210	
Phe	Tyr	Val	Leu	Gly	Val	Arg	Tyr	Leu	Thr	Leu	Thr	Phe	Thr	Cys	
				215					220					225	
Ser	Thr	Pro	Trp	Ala	Glu	Ser	Ser	Thr	Lys	Phe	Arg	His	His	Met	
				230					235					240	
Tyr	Thr	Asn	Val	Ser	Gly	Leu	Thr	Ser	Phe	Gly	Glu	Lys	Val	Val	
				245					250					255	
Glu	Glu	Leu	Asn	Arg	Leu	Gly	Met	Met	Ile	Asp	Leu	Ser	Tyr	Ala	

				260					265					270
Ser	Asp	Thr	Leu	Ile 275	Arg	Arg	Val	Leu	Glu 280	Val	Ser	Gln	Ala	Pro 285
Val	Ile	Phe	Ser	His 290	Ser	Ala	Ala	Arg	Ala 295	Val	Cys	Asp	Asn	Leu 300
Leu	Asn	Val	Pro	Asp 305	Asp	Ile	Leu	Gln	Leu 310	Leu	Lys	Asn	Gly	Gly 315
Ile	Val	Met	Val	Thr 320	Leu	Ser	Met	Gly	Val 325	Leu	Gln	Cys	Asn	Leu 330
Leu	Ala	Asn	Val	Ser 335	Thr	Val	Ala	Asp	His 340	Phe	Asp	His	Ile	Arg 345
Ala	Val	Ile	Gly	Ser 350	Glu	Phe	Ile	Gly	Ile 355	Gly	Gly	Asn	Tyr	Asp 360
Gly	Thr	Gly	Arg	Phe 365	Pro	Gln	Gly	Leu	Glu 370	Asp	Val	Ser	Thr	Tyr 375
Pro	Val	Leu	Ile	Glu 380	Glu	Leu	Leu	Ser	Arg 385	Xaa	Trp	Ser	Glu	Glu 390
Glu	Leu	Gln	Gly	Val 395	Leu	Arg	Gly	Asn	Leu 400	Leu	Arg	Val	Phe	Arg 405
Gln	Val	Glu	Lys	Val 410	Arg	Glu	Glu	Ser	Arg 415	Ala	Gln	Ser	Pro	Val 420
Glu	Ala	Glu	Phe	Pro 425	Tyr	Gly	Gln	Leu	Ser 430	Thr	Ser	Cys	His	Ser 435
His	Leu	Val	Pro	Gln 440	Asn	Gly	His	Gln	Ala 445	Thr	His	Leu	Glu	Val 450
Thr	Lys	Gln	Pro	Thr 455	Asn	Arg	Val	Pro	Trp 460	Arg	Ser	Ser	Asn	Ala 465
Ser	Pro	Tyr	Leu	Val 470	Pro	Gly	Leu	Val	Ala 475	Ala	Ala	Thr	Ile	Pro 480
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<210> 64

<212> DNA

<213> Artificial

<220>

<222> 1-25

<223> Synthetic construct.

<400> 64



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<211> 183  
<212> PRT  
<213> Homo sapiens

<400> 68  
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20 25 30  
Cys Ile Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn  
35 40 45  
Gln Asn Val Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu  
50 55 60



Pro Met Pro Val Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu  
65 70 75

Cys Glu Cys Arg Tyr Glu Glu Arg Ser Thr Thr Thr Ile Lys Val  
80 85 90

Ile Ile Val Ile Tyr Leu Ser Val Val Gly Ala Leu Leu Leu Tyr  
95 100 105

Met Ala Phe Leu Met Leu Val Asp Pro Leu Ile Arg Lys Pro Asp  
110 115 120

Ala Tyr Thr Glu Gln Leu His Asn Glu Glu Glu Asn Glu Asp Ala  
125 130 135

Arg Ser Met Ala Ala Ala Ala Ala Ser Leu Gly Gly Pro Arg Ala  
140 145 150

Asn Thr Val Leu Glu Arg Val Glu Gly Ala Gln Gln Arg Trp Lys  
155 160 165

Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe Asp Arg His Lys  
170 175 180

Met Leu Ser

<210> 69  
<211> 3170  
<212> DNA  
<213> Homo sapiens

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gtccaccctt ttaaaaatta ttatttgaag taatttattt acaggaaatg 3000  
ttaatgagat gtattttctt atagagatat ttcttacaga aagctttgta 3050  
gcagaatata tttgcagcta ttgactttgt aatttaggaa aaatgtataa 3100  
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aaaaaaaaa aaaaaaaaaa 3170

<210> 70  
<211> 259  
<212> PRT  
<213> Homo sapiens

<400> 70  
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Leu Leu Ala Ala Val Leu Met Val Glu Ser Ser Gln Ile Gly Ser  
20 25 30  
Ser Arg Ala Lys Leu Asn Ser Ile Lys Ser Ser Leu Gly Gly Glu  
35 40 45

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<210> 71

<212> DNA

<400> 71

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atatttttagt	aattcatatg	ttttagatta	taggttttaa	catacttggtg	300
aaaataacttg	atgtgtttta	aagccttggg	cagaaattct	gtattgttga	350
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<210> 72  
<211> 363  
<212> PRT  
<213> Homo sapiens

<400> 72  
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Phe Gly Glu Leu Ala Pro Pro Lys Met Ala Asn Ile Thr Ser Ser  
35 40 45  
Gln Ile Leu Asp Gln Leu Lys Ala Pro Ser Leu Gly Gln Phe Thr  
50 55 60  
Thr Thr Pro Ser Thr Gln Gln Asn Ser Thr Ser His Pro Thr Thr  
65 70 75  
Thr Thr Ser Trp Asp Leu Lys Pro Pro Thr Ser Gln Ser Ser Val  
80 85 90  
Leu Ser His Leu Asp Phe Lys Ser Gln Pro Glu Pro Ser Pro Val  
95 100 105  
Leu Ser Gln Leu Ser Gln Arg Gln Gln His Gln Ser Gln Ala Val  
110 115 120  
Thr Val Pro Pro Pro Gly Leu Glu Ser Phe Pro Ser Gln Ala Lys  
125 130 135  
Leu Arg Glu Ser Thr Pro Gly Asp Ser Pro Ser Thr Val Asn Lys  
140 145 150  
Leu Leu Gln Leu Pro Ser Thr Thr Ile Glu Asn Ile Ser Val Ser  
155 160 165  
Val His Gln Pro Gln Pro Lys His Ile Lys Leu Ala Lys Arg Arg  
170 175 180  
Ile Pro Pro Ala Ser Lys Ile Pro Ala Ser Ala Val Glu Met Pro  
185 190 195  
Gly Ser Ala Asp Val Thr Gly Leu Asn Val Gln Phe Gly Ala Leu  
200 205 210  
Glu Phe Gly Ser Glu Pro Ser Leu Ser Glu Phe Gly Ser Ala Pro  
215 220 225

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Ser	Ser	Glu	Asn	Ser	Asn	Gln	Ile	Pro	Ile	Ser	Leu	Tyr	Ser	Lys
				230					235					240
Ser	Leu	Ser	Glu	Pro	Leu	Asn	Thr	Ser	Leu	Ser	Met	Thr	Ser	Ala
				245					250					255
Val	Gln	Asn	Ser	Thr	Tyr	Thr	Thr	Ser	Val	Ile	Thr	Ser	Cys	Ser
				260					265					270
Leu	Thr	Ser	Ser	Ser	Leu	Asn	Ser	Ala	Ser	Pro	Val	Ala	Met	Ser
				275					280					285
Ser	Ser	Tyr	Asp	Gln	Ser	Ser	Val	His	Asn	Arg	Ile	Pro	Tyr	Gln
				290					295					300
Ser	Pro	Val	Ser	Ser	Ser	Glu	Ser	Ala	Pro	Gly	Thr	Ile	Met	Asn
				305					310					315
Gly	His	Gly	Gly	Gly	Arg	Ser	Gln	Gln	Thr	Leu	Asp	Ser	Lys	Tyr
				320					325					330
Ser	Ser	Lys	Leu	Leu	Leu	Ser	Trp	Leu	Val	Pro	Thr	Lys	Gln	Arg
				335					340					345
Lys	Arg	Ile	Ala	His	Val	Met	Trp	Lys	Thr	Pro	Val	Gly	Gln	Trp
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Leu	Ile	Arg												

<210> 73  
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<212> DNA  
<213> Artificial  
  
<220>  
<221> Artificial sequence  
<222> 1-26  
<223> Synthetic construct.  
  
<400> 73  
aatcatggc aaatatttcc cttccc 26  
  
<210> 74  
<211> 22  
<212> DNA  
<213> Artificial  
  
<220>  
<221> Artificial sequence  
<222> 1-22  
<223> Synthetic construct.  
  
<400> 74  
tggtaaactg gcccaaactc gg 22  
  
<210> 75  
<211> 50

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<213> Artificial

<220>  
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<400> 75  
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<210> 76  
<211> 1989  
<212> DNA  
<213> Homo sapiens

<400> 76  
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tgactcagc ggtggaggag acggacgcgg ggctgtacac ctgcaacctg 150  
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gccccctgcc tgccaagtac atcgacctag acaaagggtt ccggaaggag 1050



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 caataaagtc cccatctgat ttttaaaaaa aaaaaaaaaa 1989

<210> 77  
 <211> 341  
 <212> PRT  
 <213> Homo sapiens

<400> 77  
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 Ala Gly Leu Tyr Thr Cys Asn Leu His His His Tyr Cys His Leu  
 35 40 45  
 Tyr Glu Ser Leu Ala Val Arg Leu Glu Val Thr Asp Gly Pro Pro  
 50 55 60  
 Ala Thr Pro Ala Tyr Trp Asp Gly Glu Lys Glu Val Leu Ala Val  
 65 70 75

Ala	Arg	Gly	Ala	Pro	Ala	Leu	Leu	Thr	Cys	Val	Asn	Arg	Gly	His
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Val	Trp	Thr	Asp	Arg	His	Val	Glu	Glu	Ala	Gln	Gln	Val	Val	His
				95					100					105
Trp	Asp	Arg	Gln	Pro	Pro	Gly	Val	Pro	His	Asp	Arg	Ala	Asp	Arg
				110					115					120
Leu	Leu	Asp	Leu	Tyr	Ala	Ser	Gly	Glu	Arg	Arg	Ala	Tyr	Gly	Pro
				125					130					135
Leu	Phe	Leu	Arg	Asp	Arg	Val	Ala	Val	Gly	Ala	Asp	Ala	Phe	Glu
				140					145					150
Arg	Gly	Asp	Phe	Ser	Leu	Arg	Ile	Glu	Pro	Leu	Glu	Val	Ala	Asp
				155					160					165
Glu	Gly	Thr	Tyr	Ser	Cys	His	Leu	His	His	His	Tyr	Cys	Gly	Leu
				170					175					180
His	Glu	Arg	Arg	Val	Phe	His	Leu	Thr	Val	Ala	Glu	Pro	His	Ala
				185					190					195
Glu	Pro	Pro	Pro	Arg	Gly	Ser	Pro	Gly	Asn	Gly	Ser	Ser	His	Ser
				200					205					210
Gly	Ala	Pro	Gly	Pro	Asp	Pro	Thr	Leu	Ala	Arg	Gly	His	Asn	Val
				215					220					225
Ile	Asn	Val	Ile	Val	Pro	Glu	Ser	Arg	Ala	His	Phe	Phe	Gln	Gln
				230					235					240
Leu	Gly	Tyr	Val	Leu	Ala	Thr	Leu	Leu	Leu	Phe	Ile	Leu	Leu	Leu
				245					250					255
Val	Thr	Val	Leu	Leu	Ala	Ala	Arg	Arg	Arg	Arg	Gly	Gly	Tyr	Glu
				260					265					270
Tyr	Ser	Asp	Gln	Lys	Ser	Gly	Lys	Ser	Lys	Gly	Lys	Asp	Val	Asn
				275					280					285
Leu	Ala	Glu	Phe	Ala	Val	Ala	Ala	Gly	Asp	Gln	Met	Leu	Tyr	Arg
				290					295					300
Ser	Glu	Asp	Ile	Gln	Leu	Asp	Tyr	Lys	Asn	Asn	Ile	Leu	Lys	Glu
				305					310					315
Arg	Ala	Glu	Leu	Ala	His	Ser	Pro	Leu	Pro	Ala	Lys	Tyr	Ile	Asp
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Leu	Asp	Lys	Gly	Phe	Arg	Lys	Glu	Asn	Cys	Lys				
				335					340					

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<210> 78
<211> 2243
<212> DNA
<213> Homo sapiens
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<212> PRT  
<213> Homo sapiens

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35 40 45  
Pro Glu Asp Arg Phe Cys Gly Thr Tyr Ile Ile Phe Phe Ser Leu  
50 55 60  
Gly Ile Gly Ser Leu Leu Pro Trp Asn Phe Phe Ile Thr Ala Lys  
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Glu Tyr Trp Met Phe Lys Leu Arg Asn Ser Ser Ser Pro Ala Thr  
80 85 90  
Gly Glu Asp Pro Glu Gly Ser Asp Ile Leu Asn Tyr Phe Glu Ser  
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Tyr	Leu	Ala	Val	Ala	Ser	Thr	Val	Pro	Ser	Met	Leu	Cys	Leu	Val	110	115	120
Ala	Asn	Phe	Leu	Leu	Val	Asn	Arg	Val	Ala	Val	His	Ile	Arg	Val	125	130	135
Leu	Ala	Ser	Leu	Thr	Val	Ile	Leu	Ala	Ile	Phe	Met	Val	Ile	Thr	140	145	150
Ala	Leu	Val	Lys	Val	Asp	Thr	Ser	Ser	Trp	Thr	Arg	Gly	Phe	Phe	155	160	165
Ala	Val	Thr	Ile	Val	Cys	Met	Val	Ile	Leu	Ser	Gly	Ala	Ser	Thr	170	175	180
Val	Phe	Ser	Ser	Ser	Ile	Tyr	Gly	Met	Thr	Gly	Ser	Phe	Pro	Met	185	190	195
Arg	Asn	Ser	Gln	Ala	Leu	Ile	Ser	Gly	Gly	Ala	Met	Gly	Gly	Thr	200	205	210
Val	Ser	Ala	Val	Ala	Ser	Leu	Val	Asp	Leu	Ala	Ala	Ser	Ser	Asp	215	220	225
Val	Arg	Asn	Ser	Ala	Leu	Ala	Phe	Phe	Leu	Thr	Ala	Thr	Ile	Phe	230	235	240
Leu	Val	Leu	Cys	Met	Gly	Leu	Tyr	Leu	Leu	Leu	Ser	Arg	Leu	Glu	245	250	255
Tyr	Ala	Arg	Tyr	Tyr	Met	Arg	Pro	Val	Leu	Ala	Ala	His	Val	Phe	260	265	270
Ser	Gly	Glu	Glu	Glu	Leu	Pro	Gln	Asp	Ser	Leu	Ser	Ala	Pro	Ser	275	280	285
Val	Ala	Ser	Arg	Phe	Ile	Asp	Ser	His	Thr	Pro	Pro	Leu	Arg	Pro	290	295	300
Ile	Leu	Lys	Lys	Thr	Ala	Ser	Leu	Gly	Phe	Cys	Val	Thr	Tyr	Val	305	310	315
Phe	Phe	Ile	Thr	Ser	Leu	Ile	Tyr	Pro	Ala	Val	Cys	Thr	Asn	Ile	320	325	330
Glu	Ser	Leu	Asn	Lys	Gly	Ser	Gly	Ser	Leu	Trp	Thr	Thr	Lys	Phe	335	340	345
Phe	Ile	Pro	Leu	Thr	Thr	Phe	Leu	Leu	Tyr	Asn	Phe	Ala	Asp	Leu	350	355	360
Cys	Gly	Arg	Gln	Leu	Thr	Ala	Trp	Ile	Gln	Val	Pro	Gly	Pro	Asn	365	370	375
Ser	Lys	Ala	Leu	Pro	Gly	Phe	Val	Leu	Leu	Arg	Thr	Cys	Leu	Ile	380	385	390
Pro	Leu	Phe	Val	Leu	Cys	Asn	Tyr	Gln	Pro	Arg	Val	His	Leu	Lys			

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Thr Val Val Phe Gln Ser Asp Val Tyr Pro Ala Leu Leu Ser Ser			
	410	415	420
Leu Leu Gly Leu Ser Asn Gly Tyr Leu Ser Thr Leu Ala Leu Leu			
	425	430	435
Tyr Gly Pro Lys Ile Val Pro Arg Glu Leu Ala Glu Ala Thr Gly			
	440	445	450
Val Val Met Ser Phe Tyr Val Cys Leu Gly Leu Thr Leu Gly Ser			
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Ala Cys Ser Thr Leu Leu Val His Leu Ile			
	470	475	

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<223> Synthetic construct.

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<212> DNA

<213> Homo sapiens

<400> 83

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<211> 567

<213> Homo sapiens

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Arg Val Ile Val Val Gly Ala Gly Val Ala Gly Leu Val Ala Ala  
65 70 75

Asp Asn Arg Ile Gly Gly Arg Ile Phe Thr Tyr Arg Asp Gln Asn  
95 100 105

His Arg Ile Leu His Lys Leu Cys Gln Gly Leu Gly Leu Asn Leu  
125 130 135

Glu Val Lys Leu Arg Asn Tyr Val Val Glu Lys Val Pro Glu Lys  
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Leu	Gly	Tyr	Ala	Leu	Arg	Pro	Gln	Glu	Lys	Gly	His	Ser	Pro	Glu
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Asp	Ile	Tyr	Gln	Met	Ala	Leu	Asn	Gln	Ala	Leu	Lys	Asp	Leu	Lys
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Ala	Leu	Gly	Cys	Arg	Lys	Ala	Met	Lys	Lys	Phe	Glu	Arg	His	Thr
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Leu	Leu	Glu	Tyr	Leu	Leu	Gly	Glu	Gly	Asn	Leu	Ser	Arg	Pro	Ala
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Leu	Ser	Phe	Ala	Glu	Ala	Leu	Arg	Ala	His	Ser	Cys	Leu	Ser	Asp
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Arg	Leu	Gln	Tyr	Ser	Arg	Ile	Val	Gly	Gly	Trp	Asp	Leu	Leu	Pro
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Arg	Ala	Leu	Leu	Ser	Ser	Leu	Ser	Gly	Leu	Val	Leu	Leu	Asn	Ala
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Pro	Val	Val	Ala	Met	Thr	Gln	Gly	Pro	His	Asp	Val	His	Val	Gln
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Ile	Glu	Thr	Ser	Pro	Pro	Ala	Arg	Asn	Leu	Lys	Val	Leu	Lys	Ala
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Asp	Val	Val	Leu	Leu	Thr	Ala	Ser	Gly	Pro	Ala	Val	Lys	Arg	Ile
				320					325					330
Thr	Phe	Ser	Pro	Pro	Leu	Pro	Arg	His	Met	Gln	Glu	Ala	Leu	Arg
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Arg	Leu	His	Tyr	Val	Pro	Ala	Thr	Lys	Val	Phe	Leu	Ser	Phe	Arg
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Arg	Pro	Phe	Trp	Arg	Glu	Glu	His	Ile	Glu	Gly	Gly	His	Ser	Asn
				365					370					375
Thr	Asp	Arg	Pro	Ser	Arg	Met	Ile	Phe	Tyr	Pro	Pro	Pro	Arg	Glu
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Gly	Ala	Leu	Leu	Leu	Ala	Ser	Tyr	Thr	Trp	Ser	Asp	Ala	Ala	Ala
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Ala	Phe	Ala	Gly	Leu	Ser	Arg	Glu	Glu	Ala	Leu	Arg	Leu	Ala	Leu
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Asp	Asp	Val	Ala	Ala	Leu	His	Gly	Pro	Val	Val	Arg	Gln	Leu	Trp
				425					430					435
Asp	Gly	Thr	Gly	Val	Val	Lys	Arg	Trp	Ala	Glu	Asp	Gln	His	Ser
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Gln	Gly	Gly	Phe	Val	Val	Gln	Pro	Pro	Ala	Leu	Trp	Gln	Thr	Glu

				455					460					465
Lys	Asp	Asp	Trp	Thr 470	Val	Pro	Tyr	Gly	Arg 475	Ile	Tyr	Phe	Ala	Gly 480
Glu	His	Thr	Ala	Tyr 485	Pro	His	Gly	Trp	Val 490	Glu	Thr	Ala	Val	Lys 495
Ser	Ala	Leu	Arg	Ala 500	Ala	Ile	Lys	Ile	Asn 505	Ser	Arg	Lys	Gly	Pro 510
Ala	Ser	Asp	Thr	Ala 515	Ser	Pro	Glu	Gly	His 520	Ala	Ser	Asp	Met	Glu 525
Gly	Gln	Gly	His	Val 530	His	Gly	Val	Ala	Ser 535	Ser	Pro	Ser	His	Asp 540
Leu	Ala	Lys	Glu	Glu 545	Gly	Ser	His	Pro	Pro 550	Val	Gln	Gly	Gln	Leu 555
Ser	Leu	Gln	Asn	Thr 560	Thr	His	Thr	Arg	Thr 565	Ser	His			

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<211> 3316
<212> DNA
<213> Homo sapiens
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<211> 739

<212> PRT

<213> Homo sapiens

<400> 86

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			20					25						30

Gly	Ser	Pro	His	Ser	Leu	Glu	Ala	Leu	Arg	Asp	Ala	Ala	Pro	Ser		35	40	45
Gln	Gly	Leu	Asn	Phe	Leu	Leu	Leu	Phe	Thr	Lys	Met	Leu	Phe	Ile		50	55	60
Phe	Asn	Phe	Leu	Phe	Ser	Pro	Leu	Pro	Thr	Pro	Ala	Leu	Ile	Cys		65	70	75
Ile	Leu	Thr	Phe	Gly	Ala	Ala	Ile	Phe	Leu	Trp	Leu	Ile	Thr	Arg		80	85	90
Pro	Gln	Pro	Val	Leu	Pro	Leu	Leu	Asp	Leu	Asn	Asn	Gln	Ser	Val		95	100	105
Gly	Ile	Glu	Gly	Gly	Ala	Arg	Lys	Gly	Val	Ser	Gln	Lys	Asn	Asn		110	115	120
Asp	Leu	Thr	Ser	Cys	Cys	Phe	Ser	Asp	Ala	Lys	Thr	Met	Tyr	Glu		125	130	135
Val	Phe	Gln	Arg	Gly	Leu	Ala	Val	Ser	Asp	Asn	Gly	Pro	Cys	Leu		140	145	150
Gly	Tyr	Arg	Lys	Pro	Asn	Gln	Pro	Tyr	Arg	Trp	Leu	Ser	Tyr	Lys		155	160	165
Gln	Val	Ser	Asp	Arg	Ala	Glu	Tyr	Leu	Gly	Ser	Cys	Leu	Leu	His		170	175	180
Lys	Gly	Tyr	Lys	Ser	Ser	Pro	Asp	Gln	Phe	Val	Gly	Ile	Phe	Ala		185	190	195
Gln	Asn	Arg	Pro	Glu	Trp	Ile	Ile	Ser	Glu	Leu	Ala	Cys	Tyr	Thr		200	205	210
Tyr	Ser	Met	Val	Ala	Val	Pro	Leu	Tyr	Asp	Thr	Leu	Gly	Pro	Glu		215	220	225
Ala	Ile	Val	His	Ile	Val	Asn	Lys	Ala	Asp	Ile	Ala	Met	Val	Ile		230	235	240
Cys	Asp	Thr	Pro	Gln	Lys	Ala	Leu	Val	Leu	Ile	Gly	Asn	Val	Glu		245	250	255
Lys	Gly	Phe	Thr	Pro	Ser	Leu	Lys	Val	Ile	Ile	Leu	Met	Asp	Pro		260	265	270
Phe	Asp	Asp	Asp	Leu	Lys	Gln	Arg	Gly	Glu	Lys	Ser	Gly	Ile	Glu		275	280	285
Ile	Leu	Ser	Leu	Tyr	Asp	Ala	Glu	Asn	Leu	Gly	Lys	Glu	His	Phe		290	295	300
Arg	Lys	Pro	Val	Pro	Pro	Ser	Pro	Glu	Asp	Leu	Ser	Val	Ile	Cys		305	310	315
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Glu His Ala Tyr Glu Pro Thr Pro Asp	Asp Val Ala Ile Ser Tyr	
350	355	360
Leu Pro Leu Ala His Met Phe Glu Arg	Ile Val Gln Ala Val Val	
365	370	375
Tyr Ser Cys Gly Ala Arg Val Gly Phe	Phe Gln Gly Asp Ile Arg	
380	385	390
Leu Leu Ala Asp Asp Met Lys Thr Leu	Lys Pro Thr Leu Phe Pro	
395	400	405
Ala Val Pro Arg Leu Leu Asn Arg Ile	Tyr Asp Lys Val Gln Asn	
410	415	420
Glu Ala Lys Thr Pro Leu Lys Lys Phe	Leu Leu Lys Leu Ala Val	
425	430	435
Ser Ser Lys Phe Lys Glu Leu Gln Lys	Gly Ile Ile Arg His Asp	
440	445	450
Ser Phe Trp Asp Lys Leu Ile Phe Ala	Lys Ile Gln Asp Ser Leu	
455	460	465
Gly Gly Arg Val Arg Val Ile Val Thr	Gly Ala Ala Pro Met Ser	
470	475	480
Thr Ser Val Met Thr Phe Phe Arg Ala	Ala Met Gly Cys Gln Val	
485	490	495
Tyr Glu Ala Tyr Gly Gln Thr Glu Cys	Thr Gly Gly Cys Thr Phe	
500	505	510
Thr Leu Pro Gly Asp Trp Thr Ser Gly	His Val Gly Val Pro Leu	
515	520	525
Ala Cys Asn Tyr Val Lys Leu Glu Asp	Val Ala Asp Met Asn Tyr	
530	535	540
Phe Thr Val Asn Asn Glu Gly Glu Val	Cys Ile Lys Gly Thr Asn	
545	550	555
Val Phe Lys Gly Tyr Leu Lys Asp Pro	Glu Lys Thr Gln Glu Ala	
560	565	570
Leu Asp Ser Asp Gly Trp Leu His Thr	Gly Asp Ile Gly Arg Trp	
575	580	585
Leu Pro Asn Gly Thr Leu Lys Ile Ile	Asp Arg Lys Lys Asn Ile	
590	595	600
Phe Lys Leu Ala Gln Gly Glu Tyr Ile	Ala Pro Glu Lys Ile Glu	
605	610	615

Asn	Ile	Tyr	Asn	Arg	Ser	Gln	Pro	Val	Leu	Gln	Ile	Phe	Val	His
				620					625					630
Gly	Glu	Ser	Leu	Arg	Ser	Ser	Leu	Val	Gly	Val	Val	Val	Pro	Asp
				635					640					645
Thr	Asp	Val	Leu	Pro	Ser	Phe	Ala	Ala	Lys	Leu	Gly	Val	Lys	Gly
				650					655					660
Ser	Phe	Glu	Glu	Leu	Cys	Gln	Asn	Gln	Val	Val	Arg	Glu	Ala	Ile
				665					670					675
Leu	Glu	Asp	Leu	Gln	Lys	Ile	Gly	Lys	Glu	Ser	Gly	Leu	Lys	Thr
				680					685					690
Phe	Glu	Gln	Val	Lys	Ala	Ile	Phe	Leu	His	Pro	Glu	Pro	Phe	Ser
				695					700					705
Ile	Glu	Asn	Gly	Leu	Leu	Thr	Pro	Thr	Leu	Lys	Ala	Lys	Arg	Gly
				710					715					720
Glu	Leu	Ser	Lys	Tyr	Phe	Arg	Thr	Gln	Ile	Asp	Ser	Leu	Tyr	Glu
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His	Ile	Gln	Asp											

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 <212> DNA  
 <213> Homo sapiens

<400> 87  
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 ccaggacatt ggtgaccgcg caatccggta tggacgactg gaagcccagc 150  
 cccctcatca agcccttttg ggctcggaag aagcggagct ggtaccttac 200  
 ctggaagtat aaactgacaa accagcgggc cctgcggaga ttctgtcaga 250  
 caggggccgt gcttttctct ctggtgactg tcattgtcaa tatcaagttg 300  
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 gaggcagtgg tccccggcgg gtccctggacg tagaggtgta ttcaagtcgc 450  
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 ccgggagcag ggccggggca tccatgtcat tgtcctcaac caggccacgg 550  
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Leu	Asn	Gln	Ala	Thr 140	Gly	His	Val	Met	Ala 145	Lys	Arg	Val	Phe	Asp 150
Thr	Tyr	Ser	Pro	His 155	Glu	Asp	Glu	Ala	Met 160	Val	Leu	Phe	Leu	Asn 165
Met	Val	Ala	Pro	Gly 170	Arg	Val	Leu	Ile	Cys 175	Thr	Val	Lys	Asp	Glu 180
Gly	Ser	Phe	His	Leu 185	Lys	Asp	Thr	Ala	Lys 190	Ala	Leu	Leu	Arg	Ser 195
Leu	Gly	Ser	Gln	Ala 200	Gly	Pro	Ala	Leu	Gly 205	Trp	Arg	Asp	Thr	Trp 210
Ala	Phe	Val	Gly	Arg 215	Lys	Gly	Gly	Pro	Val 220	Phe	Gly	Glu	Lys	His 225
Ser	Lys	Ser	Pro	Ala 230	Leu	Ser	Ser	Trp	Gly 235	Asp	Pro	Val	Leu	Leu 240
Lys	Thr	Asp	Val	Pro 245	Leu	Ser	Ser	Ala	Glu 250	Glu	Ala	Glu	Cys	His 255
Trp	Ala	Asp	Thr	Glu 260	Leu	Asn	Arg	Arg	Arg 265	Arg	Arg	Phe	Cys	Ser 270
Lys	Val	Glu	Gly	Tyr 275	Gly	Ser	Val	Cys	Ser 280	Cys	Lys	Asp	Pro	Thr 285
Pro	Ile	Glu	Phe	Ser 290	Pro	Asp	Pro	Leu	Pro 295	Asp	Asn	Lys	Val	Leu 300
Asn	Val	Pro	Val	Ala 305	Val	Ile	Ala	Gly	Asn 310	Arg	Pro	Asn	Tyr	Leu 315
Tyr	Arg	Met	Leu	Arg 320	Ser	Leu	Leu	Ser	Ala 325	Gln	Gly	Val	Ser	Pro 330
Gln	Met	Ile	Thr	Val 335	Phe	Ile	Asp	Gly	Tyr 340	Tyr	Glu	Glu	Pro	Met 345
Asp	Val	Val	Ala	Leu 350	Phe	Gly	Leu	Arg	Gly 355	Ile	Gln	His	Thr	Pro 360
Ile	Ser	Ile	Lys	Asn 365	Ala	Arg	Val	Ser	Gln 370	His	Tyr	Lys	Ala	Ser 375
Leu	Thr	Ala	Thr	Phe 380	Asn	Leu	Phe	Pro	Glu 385	Ala	Lys	Phe	Ala	Val 390
Val	Leu	Glu	Glu	Asp 395	Leu	Asp	Ile	Ala	Val 400	Asp	Phe	Phe	Ser	Phe 405
Leu	Ser	Gln	Ser	Ile 410	His	Leu	Leu	Glu	Glu 415	Asp	Asp	Ser	Leu	Tyr 420
Cys	Ile	Ser	Ala	Trp	Asn	Asp	Gln	Gly	Tyr	Glu	His	Thr	Ala	Glu

425	430	435
Asp Pro Ala Leu Leu Tyr Arg Val Glu Thr Met Pro Gly Leu Gly 440	445	450
Trp Val Leu Arg Arg Ser Leu Tyr Lys Glu Glu Leu Glu Pro Lys 455	460	465
Trp Pro Thr Pro Glu Lys Leu Trp Asp Trp Asp Met Trp Met Arg 470	475	480
Met Pro Glu Gln Arg Arg Gly Arg Glu Cys Ile Ile Pro Asp Val 485	490	495
Ser Arg Ser Tyr His Phe Gly Ile Val Gly Leu Asn Met Asn Gly 500	505	510
Tyr Phe His Glu Ala Tyr Phe Lys Lys His Lys Phe Asn Thr Val 515	520	525
Pro Gly Val Gln Leu Arg Asn Val Asp Ser Leu Lys Lys Glu Ala 530	535	540
Tyr Glu Val Glu Val His Arg Leu Leu Ser Glu Ala Glu Val Leu 545	550	555
Asp His Ser Lys Asn Pro Cys Glu Asp Ser Phe Leu Pro Asp Thr 560	565	570
Glu Gly His Thr Tyr Val Ala Phe Ile Arg Met Glu Lys Asp Asp 575	580	585
Asp Phe Thr Thr Trp Thr Gln Leu Ala Lys Cys Leu His Ile Trp 590	595	600
Asp Leu Asp Val Arg Gly Asn His Arg Gly Leu Trp Arg Leu Phe 605	610	615
Arg Lys Lys Asn His Phe Leu Val Val Gly Val Pro Ala Ser Pro 620	625	630
Tyr Ser Val Lys Lys Pro Pro Ser Val Thr Pro Ile Phe Leu Glu 635	640	645
Pro Pro Pro Lys Glu Glu Gly Ala Pro Gly Ala Pro Glu Gln Thr 650	655	660

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<211> 25

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<220>

<221> Artificial sequence

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<223> Synthetic construct.

<400> 89

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<400> 91  
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<210> 92  
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<400> 93  
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<210> 94  
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 <212> DNA  
 <213> Homo sapiens

[illegible]

**E**



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 ttgtcaaata aatagcagat tgtagtgtca aaaaaaa 3037

<210> 95  
 <211> 307  
 <212> PRT  
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<400> 95

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Ser	Glu	Glu	Arg	Leu	Lys	Leu	Val	Thr	Val	Leu	Gly	Ala	Gly	Leu
				35				40					45	
Leu	Cys	Gly	Thr	Ala	Leu	Ala	Val	Ile	Val	Pro	Glu	Gly	Val	His
				50				55					60	
Ala	Leu	Tyr	Glu	Asp	Ile	Leu	Glu	Gly	Lys	His	His	Gln	Ala	Ser
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Glu	Thr	His	Asn	Val	Ile	Ala	Ser	Asp	Lys	Ala	Ala	Glu	Lys	Ser
				80				85					90	
Val	Val	His	Glu	His	Glu	His	Ser	His	Asp	His	Thr	Gln	Leu	His
				95				100					105	
Ala	Tyr	Ile	Gly	Val	Ser	Leu	Val	Leu	Gly	Phe	Val	Phe	Met	Leu
				110				115					120	
Leu	Val	Asp	Gln	Ile	Gly	Asn	Ser	His	Val	His	Ser	Thr	Asp	Asp
				125				130					135	
Pro	Glu	Ala	Ala	Arg	Ser	Ser	Asn	Ser	Lys	Ile	Thr	Thr	Thr	Leu
				140				145					150	
Gly	Leu	Val	Val	His	Ala	Ala	Ala	Asp	Gly	Val	Ala	Leu	Gly	Ala
				155				160					165	
Ala	Ala	Ser	Thr	Ser	Gln	Thr	Ser	Val	Gln	Leu	Ile	Val	Phe	Val
				170				175					180	
Ala	Ile	Met	Leu	His	Lys	Ala	Pro	Ala	Ala	Phe	Gly	Leu	Val	Ser
				185				190					195	
Phe	Leu	Met	His	Ala	Gly	Leu	Glu	Arg	Asn	Arg	Ile	Arg	Lys	His
				200				205					210	
Leu	Leu	Val	Phe	Ala	Leu	Ala	Ala	Pro	Val	Met	Ser	Met	Val	Thr
				215				220					225	
Tyr	Leu	Gly	Leu	Ser	Lys	Ser	Ser	Lys	Glu	Ala	Leu	Ser	Glu	Val

T0903T 09/3000T

	230	235	240
Asn Ala Thr Gly	Val Ala Met Leu Phe	Ser Ala Gly Thr Phe	Leu
	245	250	255
Tyr Val Ala Thr	Val His Val Leu Pro	Glu Val Gly Gly Ile	Gly
	260	265	270
His Ser His Lys	Pro Asp Ala Thr Gly	Gly Arg Gly Leu Ser	Arg
	275	280	285
Leu Glu Val Ala	Ala Leu Val Leu Gly	Cys Leu Ile Pro Leu	Ile
	290	295	300
Leu Ser Val Gly	His Gln His		
	305		

<210> 96  
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<213> Artificial  
  
<220>  
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<222> 1-25  
<223> Synthetic construct.  
  
<400> 96  
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<210> 97  
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<223> Synthetic construct.  
  
<400> 97  
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<212> DNA

<213> Homo sapiens

<400> 99

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<210> 100

<211> 401

<212> PRT

<213> Homo sapiens

<400> 100

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20 25 30

Asn Tyr Trp Ile Ala Ser Ser Arg Ser Val Asp Leu Gln Thr Arg  
35 40 45

Ile Met Glu Leu Glu Gly Arg Val Arg Arg Ala Ala Ala Glu Arg  
50 55 60

Gly Ala Val Glu Leu Lys Lys Asn Glu Phe Gln Gly Glu Leu Glu  
65 70 75

Lys Gln Arg Glu Gln Leu Asp Lys Ile Gln Ser Ser His Asn Phe  
80 85 90

Gln Leu Glu Ser Val Asn Lys Leu Tyr Gln Asp Glu Lys Ala Val  
95 100 105

Leu Val Asn Asn Ile Thr Thr Gly Glu Arg Leu Ile Arg Val Leu  
110 115 120

Gln Asp Gln Leu Lys Thr Leu Gln Arg Asn Tyr Gly Arg Leu Gln  
125 130 135

Gln Asp Val Leu Gln Phe Gln Lys Asn Gln Thr Asn Leu Glu Arg  
140 145 150

Lys Phe Ser Tyr Asp Leu Ser Gln Cys Ile Asn Gln Met Lys Glu  
155 160 165

Val Lys Glu Gln Cys Glu Glu Arg Ile Glu Glu Val Thr Lys Lys  
170 175 180

Gly Asn Glu Ala Val Ala Ser Arg Asp Leu Ser Glu Asn Asn Asp  
185 190 195

Gln Arg Gln Gln Leu Gln Ala Leu Ser Glu Pro Gln Pro Arg Leu  
200 205 210

Gln Ala Ala Gly Leu Pro His Thr Glu Val Pro Gln Gly Lys Gly  
215 220 225

Asn Val Leu Gly Asn Ser Lys Ser Gln Thr Pro Ala Pro Ser Ser  
230 235 240

Glu Val Val Leu	Asp Ser Lys Arg Gln	Val Glu Lys Glu Glu Thr	245	250	255
Asn Glu Ile Gln	Val Val Asn Glu Glu	Pro Gln Arg Asp Arg Leu	260	265	270
Pro Gln Glu Pro	Gly Arg Glu Gln Val	Val Glu Asp Arg Pro Val	275	280	285
Gly Gly Arg Gly	Phe Gly Gly Ala Gly	Glu Leu Gly Gln Thr Pro	290	295	300
Gln Val Gln Ala	Ala Leu Ser Val Ser	Gln Glu Asn Pro Glu Met	305	310	315
Glu Gly Pro Glu	Arg Asp Gln Leu Val	Ile Pro Asp Gly Gln Glu	320	325	330
Glu Glu Gln Glu	Ala Ala Gly Glu Gly	Arg Asn Gln Gln Lys Leu	335	340	345
Arg Gly Glu Asp	Asp Tyr Asn Met Asp	Glu Asn Glu Ala Glu Ser	350	355	360
Glu Thr Asp Lys	Gln Ala Ala Leu Ala	Gly Asn Asp Arg Asn Ile	365	370	375
Asp Val Phe Asn	Val Glu Asp Gln Lys	Arg Asp Thr Ile Asn Leu	380	385	390
Leu Asp Gln Arg	Glu Lys Arg Asn His	Thr Leu	395	400	

<210> 101  
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 <212> DNA  
 <213> Homo sapiens

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<210> 102  
 <211> 1089  
 <212> PRT  
 <213> Homo sapiens

<400> 102

Met	Gln	Lys	Ala	Ser	Val	Leu	Leu	Phe	Leu	Ala	Trp	Val	Cys	Phe	
1				5					10					15	
Leu	Phe	Tyr	Ala	Gly	Ile	Ala	Leu	Phe	Thr	Ser	Gly	Phe	Leu	Leu	
				20					25					30	
Thr	Arg	Leu	Glu	Leu	Thr	Asn	His	Ser	Ser	Cys	Gln	Glu	Pro	Pro	
				35					40					45	
Gly	Pro	Gly	Ser	Leu	Pro	Trp	Gly	Ser	Gln	Gly	Lys	Pro	Gly	Ala	
				50					55					60	
Cys	Trp	Met	Ala	Ser	Arg	Phe	Ser	Arg	Val	Val	Leu	Val	Leu	Ile	
				65					70					75	
Asp	Ala	Leu	Arg	Phe	Asp	Phe	Ala	Gln	Pro	Gln	His	Ser	His	Val	
				80					85					90	
Pro	Arg	Glu	Pro	Pro	Val	Ser	Leu	Pro	Phe	Leu	Gly	Lys	Leu	Ser	
				95					100					105	
Ser	Leu	Gln	Arg	Ile	Leu	Glu	Ile	Gln	Pro	His	His	Ala	Arg	Leu	
				110					115					120	
Tyr	Arg	Ser	Gln	Val	Asp	Pro	Pro	Thr	Thr	Thr	Met	Gln	Arg	Leu	
				125					130					135	
Lys	Ala	Leu	Thr	Thr	Gly	Ser	Leu	Pro	Thr	Phe	Ile	Asp	Ala	Gly	
				140					145					150	
Ser	Asn	Phe	Ala	Ser	His	Ala	Ile	Val	Glu	Asp	Asn	Leu	Ile	Lys	
				155					160					165	
Gln	Leu	Thr	Ser	Ala	Gly	Arg	Arg	Val	Val	Phe	Met	Gly	Asp	Asp	
				170					175					180	
Thr	Trp	Lys	Asp	Leu	Phe	Pro	Gly	Ala	Phe	Ser	Lys	Ala	Phe	Phe	
				185					190					195	
Phe	Pro	Ser	Phe	Asn	Val	Arg	Asp	Leu	Asp	Thr	Val	Asp	Asn	Gly	

				200					205					210
Ile	Leu	Glu	His	Leu 215	Tyr	Pro	Thr	Met	Asp 220	Ser	Gly	Glu	Trp	Asp 225
Val	Leu	Ile	Ala	His 230	Phe	Leu	Gly	Val	Asp 235	His	Cys	Gly	His	Lys 240
His	Gly	Pro	His	His 245	Pro	Glu	Met	Ala	Lys 250	Lys	Leu	Ser	Gln	Met 255
Asp	Gln	Val	Ile	Gln 260	Gly	Leu	Val	Glu	Arg 265	Leu	Glu	Asn	Asp	Thr 270
Leu	Leu	Val	Val	Ala 275	Gly	Asp	His	Gly	Met 280	Thr	Thr	Asn	Gly	Asp 285
His	Gly	Gly	Asp	Ser 290	Glu	Leu	Glu	Val	Ser 295	Ala	Ala	Leu	Phe	Leu 300
Tyr	Ser	Pro	Thr	Ala 305	Val	Phe	Pro	Ser	Thr 310	Pro	Pro	Glu	Glu	Pro 315
Glu	Val	Ile	Pro	Gln 320	Val	Ser	Leu	Val	Pro 325	Thr	Leu	Ala	Leu	Leu 330
Leu	Gly	Leu	Pro	Ile 335	Pro	Phe	Gly	Asn	Ile 340	Gly	Glu	Val	Met	Ala 345
Glu	Leu	Phe	Ser	Gly 350	Gly	Glu	Asp	Ser	Gln 355	Pro	His	Ser	Ser	Ala 360
Leu	Ala	Gln	Ala	Ser 365	Ala	Leu	His	Leu	Asn 370	Ala	Gln	Gln	Val	Ser 375
Arg	Phe	Leu	His	Thr 380	Tyr	Ser	Ala	Ala	Thr 385	Gln	Asp	Leu	Gln	Ala 390
Lys	Glu	Leu	His	Gln 395	Leu	Gln	Asn	Leu	Phe 400	Ser	Lys	Ala	Ser	Ala 405
Asp	Tyr	Gln	Trp	Leu 410	Leu	Gln	Ser	Pro	Lys 415	Gly	Ala	Glu	Ala	Thr 420
Leu	Pro	Thr	Val	Ile 425	Ala	Glu	Leu	Gln	Gln 430	Phe	Leu	Arg	Gly	Ala 435
Arg	Ala	Met	Cys	Ile 440	Glu	Ser	Trp	Ala	Arg 445	Phe	Ser	Leu	Val	Arg 450
Met	Ala	Gly	Gly	Thr 455	Ala	Leu	Leu	Ala	Ala 460	Ser	Cys	Phe	Ile	Cys 465
Leu	Leu	Ala	Ser	Gln 470	Trp	Ala	Ile	Ser	Pro 475	Gly	Phe	Pro	Phe	Cys 480
Pro	Leu	Leu	Leu	Thr 485	Pro	Val	Ala	Trp	Gly 490	Leu	Val	Gly	Ala	Ile 495

Ala	Tyr	Ala	Gly	Leu	Leu	Gly	Thr	Ile	Glu	Leu	Lys	Leu	Asp	Leu
				500					505					510
Val	Leu	Leu	Gly	Ala	Val	Ala	Ala	Val	Ser	Ser	Phe	Leu	Pro	Phe
				515					520					525
Leu	Trp	Lys	Ala	Trp	Ala	Gly	Trp	Gly	Ser	Lys	Arg	Pro	Leu	Ala
				530					535					540
Thr	Leu	Phe	Pro	Ile	Pro	Gly	Pro	Val	Leu	Leu	Leu	Leu	Leu	Phe
				545					550					555
Arg	Leu	Ala	Val	Phe	Phe	Ser	Asp	Ser	Phe	Val	Val	Ala	Glu	Ala
				560					565					570
Arg	Ala	Thr	Pro	Phe	Leu	Leu	Gly	Ser	Phe	Ile	Leu	Leu	Leu	Val
				575					580					585
Val	Gln	Leu	His	Trp	Glu	Gly	Gln	Leu	Leu	Pro	Pro	Lys	Leu	Leu
				590					595					600
Thr	Met	Pro	Arg	Leu	Gly	Thr	Ser	Ala	Thr	Thr	Asn	Pro	Pro	Arg
				605					610					615
His	Asn	Gly	Ala	Tyr	Ala	Leu	Arg	Leu	Gly	Ile	Gly	Leu	Leu	Leu
				620					625					630
Cys	Thr	Arg	Leu	Ala	Gly	Leu	Phe	His	Arg	Cys	Pro	Glu	Glu	Thr
				635					640					645
Pro	Val	Cys	His	Ser	Ser	Pro	Trp	Leu	Ser	Pro	Leu	Ala	Ser	Met
				650					655					660
Val	Gly	Gly	Arg	Ala	Lys	Asn	Leu	Trp	Tyr	Gly	Ala	Cys	Val	Ala
				665					670					675
Ala	Leu	Val	Ala	Leu	Leu	Ala	Ala	Val	Arg	Leu	Trp	Leu	Arg	Arg
				680					685					690
Tyr	Gly	Asn	Leu	Lys	Ser	Pro	Glu	Pro	Pro	Met	Leu	Phe	Val	Arg
				695					700					705
Trp	Gly	Leu	Pro	Leu	Met	Ala	Leu	Gly	Thr	Ala	Ala	Tyr	Trp	Ala
				710					715					720
Leu	Ala	Ser	Gly	Ala	Asp	Glu	Ala	Pro	Pro	Arg	Leu	Arg	Val	Leu
				725					730					735
Val	Ser	Gly	Ala	Ser	Met	Val	Leu	Pro	Arg	Ala	Val	Ala	Gly	Leu
				740					745					750
Ala	Ala	Ser	Gly	Leu	Ala	Leu	Leu	Leu	Trp	Lys	Pro	Val	Thr	Val
				755					760					765
Leu	Val	Lys	Ala	Gly	Ala	Gly	Ala	Pro	Arg	Thr	Arg	Thr	Val	Leu
				770					775					780
Thr	Pro	Phe	Ser	Gly	Pro	Pro	Thr	Ser	Gln	Ala	Asp	Leu	Asp	Tyr



	785	790	795
Val Val Pro Gln	Ile Tyr Arg His Met	Gln Glu Glu Phe Arg	Gly
	800	805	810
Arg Leu Glu Arg	Thr Lys Ser Gln Gly	Pro Leu Thr Val Ala	Ala
	815	820	825
Tyr Gln Leu Gly	Ser Val Tyr Ser Ala	Ala Met Val Thr Ala	Leu
	830	835	840
Thr Leu Leu Ala	Phe Pro Leu Leu Leu	Leu His Ala Glu Arg	Ile
	845	850	855
Ser Leu Val Phe	Leu Leu Leu Phe Leu	Gln Ser Phe Leu Leu	Leu
	860	865	870
His Leu Leu Ala	Ala Gly Ile Pro Val	Thr Thr Pro Gly Pro	Phe
	875	880	885
Thr Val Pro Trp	Gln Ala Val Ser Ala	Trp Ala Leu Met Ala	Thr
	890	895	900
Gln Thr Phe Tyr	Ser Thr Gly His Gln	Pro Val Phe Pro Ala	Ile
	905	910	915
His Trp His Ala	Ala Phe Val Gly Phe	Pro Glu Gly His Gly	Ser
	920	925	930
Cys Thr Trp Leu	Pro Ala Leu Leu Val	Gly Ala Asn Thr Phe	Ala
	935	940	945
Ser His Leu Leu	Phe Ala Val Gly Cys	Pro Leu Leu Leu Leu	Trp
	950	955	960
Pro Phe Leu Cys	Glu Ser Gln Gly Leu	Arg Lys Arg Gln Gln	Pro
	965	970	975
Pro Gly Asn Glu	Ala Asp Ala Arg Val	Arg Pro Glu Glu Glu	Glu
	980	985	990
Glu Pro Leu Met	Glu Met Arg Leu Arg	Asp Ala Pro Gln His	Phe
	995	1000	1005
Tyr Ala Ala Leu	Leu Gln Leu Gly Leu	Lys Tyr Leu Phe Ile	Leu
	1010	1015	1020
Gly Ile Gln Ile	Leu Ala Cys Ala Leu	Ala Ala Ser Ile Leu	Arg
	1025	1030	1035
Arg His Leu Met	Val Trp Lys Val Phe	Ala Pro Lys Phe Ile	Phe
	1040	1045	1050
Glu Ala Val Gly	Phe Ile Val Ser Ser	Val Gly Leu Leu Leu	Gly
	1055	1060	1065
Ile Ala Leu Val	Met Arg Val Asp Gly	Ala Val Ser Ser Trp	Phe
	1070	1075	1080

Arg Gln Leu Phe Leu Ala Gln Gln Arg  
1085

<210> 103  
<211> 1743  
<212> DNA  
<213> Homo sapiens

<400> 103  
tgccgctgcc gccgctgctg ctgttgctcc tggcggcgcc ttggggacgg 50  
gcagttccct gtgtctctgg tggtttgcct aaacctgcaa acatcacctt 100  
cttatccatc aacatgaaga atgtcctaca atggactcca ccagaggggtc 150  
ttcaaggagt taaagttact tacactgtgc agtatttcat cacaaattgg 200  
cccaccagag gtggcactga ctacagatga gaagtccatt tctgttgtcc 250  
tgacagctcc agagaagtgg aagagaaatc cagaagacct tcctgtttcc 300  
atgcaacaaa tatactccaa totgaagtat aacgtgtctg tgttgaatac 350  
taaatacaaac agaactgtgt cccagtgtgt gaccaaccac acgctgggtgc 400  
tcacctggct ggagccgaac actctttact gcgtacacgt ggagtccttc 450  
gtcccagggc cccctcgccg tgctcagcct tctgagaagc agtgtgccag 500  
gactttgaaa gatcaatcat cagagttcaa ggctaaaatc atcttctggt 550  
atgttttgcc catatctatt accgtgtttc ttttttctgt gatgggctat 600  
tccatctacc gatatatcca cgttggcaaa gagaaacacc cagcaaattt 650  
gattttgatt tatggaaatg aatttgacaa aagattcttt gtgcctgctg 700  
aaaaaatcgt gattaacttt atcacctca atatctcgga tgattctaaa 750  
atttctcatc aggatatgag tttactggga aaaagcagtg atgtatccag 800  
ccttaatgat cctcagccca gcgggaacct gaggccccct caggaggaag 850  
aggaggtgaa acatttaggg tatgcttcgc atttgatgga aattttttgt 900  
gactctgaag aaaacacgga aggtacttct ctcaccacgc aagagtcctt 950  
cagcagaaca atacccccgg ataaaacagt cattgaatat gaatatgatg 1000  
tcagaaccac tgacatttgt gcggggcctg aagagcagga gctcagtttg 1050  
caggaggagg tgtccacaca aggaacatta ttggagtcgc aggcagcgtt 1100  
ggcagtcttg ggcccgcgaa cgttacagta ctcatacacc cctcagctcc 1150  
aagacttaga cccctggcg caggagcaca cagactcgga ggagggggccg 1200  
gaggaagagc catcgacgac cctggtcgac tgggatcccc aaactggcag 1250



Ile	His	Val	Gly	Lys 170	Glu	Lys	His	Pro	Ala 175	Asn	Leu	Ile	Leu	Ile 180
Tyr	Gly	Asn	Glu	Phe 185	Asp	Lys	Arg	Phe	Phe 190	Val	Pro	Ala	Glu	Lys 195
Ile	Val	Ile	Asn	Phe 200	Ile	Thr	Leu	Asn	Ile 205	Ser	Asp	Asp	Ser	Lys 210
Ile	Ser	His	Gln	Asp 215	Met	Ser	Leu	Leu	Gly 220	Lys	Ser	Ser	Asp	Val 225
Ser	Ser	Leu	Asn	Asp 230	Pro	Gln	Pro	Ser	Gly 235	Asn	Leu	Arg	Pro	Pro 240
Gln	Glu	Glu	Glu	Glu 245	Val	Lys	His	Leu	Gly 250	Tyr	Ala	Ser	His	Leu 255
Met	Glu	Ile	Phe	Cys 260	Asp	Ser	Glu	Glu	Asn 265	Thr	Glu	Gly	Thr	Ser 270
Leu	Thr	Gln	Gln	Glu 275	Ser	Leu	Ser	Arg	Thr 280	Ile	Pro	Pro	Asp	Lys 285
Thr	Val	Ile	Glu	Tyr 290	Glu	Tyr	Asp	Val	Arg 295	Thr	Thr	Asp	Ile	Cys 300
Ala	Gly	Pro	Glu	Glu 305	Gln	Glu	Leu	Ser	Leu 310	Gln	Glu	Glu	Val	Ser 315
Thr	Gln	Gly	Thr	Leu 320	Leu	Glu	Ser	Gln	Ala 325	Ala	Leu	Ala	Val	Leu 330
Gly	Pro	Gln	Thr	Leu 335	Gln	Tyr	Ser	Tyr	Thr 340	Pro	Gln	Leu	Gln	Asp 345
Leu	Asp	Pro	Leu	Ala 350	Gln	Glu	His	Thr	Asp 355	Ser	Glu	Glu	Gly	Pro 360
Glu	Glu	Glu	Pro	Ser 365	Thr	Thr	Leu	Val	Asp 370	Trp	Asp	Pro	Gln	Thr 375
Gly	Arg	Leu	Cys	Ile 380	Pro	Ser	Leu	Ser	Ser 385	Phe	Asp	Gln	Asp	Ser 390
Glu	Gly	Cys	Glu	Pro 395	Ser	Glu	Gly	Asp	Gly 400	Leu	Gly	Glu	Glu	Gly 405
Leu	Leu	Ser	Arg	Leu 410	Tyr	Glu	Glu	Pro	Ala 415	Pro	Asp	Arg	Pro	Pro 420
Gly	Glu	Asn	Glu	Thr 425	Tyr	Leu	Met	Gln	Phe 430	Met	Glu	Glu	Trp	Gly 435
Leu	Tyr	Val	Gln	Met 440	Glu	Asn								

118



<222> 1-51  
<223> Synthetic construct.

<400> 109  
ggacgggcag ttccctgtgt ctctggtggt ttgcctaaac ctgcaaacat 50  
c 51

<210> 110  
<211> 1114  
<212> DNA  
<213> Homo sapiens

<400> 110  
cggacgcgtg ggcggaacgc tgggcggacg cgtgggtctc tgcggggaga 50  
cgccagcctg cgtctgccat ggggctcggg ttgaggggct ggggacgtcc 100  
tctgctgact gtggccaccg ccctgatgct gcccgatgaag cccccgcag 150  
gctcctgggg ggcccagatc atcgggggac acgaggtgac cccccactcc 200  
aggccctaca tggcatccgt gcgcttcggg ggccaacatc actgcggagg 250  
cttcctgctg cgagcccgtt ggggtggtctc ggccgcccac tgcttcagcc 300  
acagagacct ccgcaactggc ctggtggtgc tgggcgcca cgtcctgagt 350  
actgcggagc ccaccagca ggtgtttggc atcgatgctc tcaccacgca 400  
ccccgactac caccatga cccacgcaa cgacatctgc ctgctgcggc 450  
tgaacggctc tgctgtcctg ggccctgcag tggggctgct gaggtgcca 500  
gggagaaggg ccaggcccc caccgagggg acacggtgcc ggggtggctgg 550  
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tgttcagggt tggggtggga cgggcagcgg tggggcacac ccattccaca 1050  
tgcaaagggc agaagcaaac ccagtaaaat gttaactgac aaaaaaaaaa 1100

aaaaaaaaaa gaaa 1114

<210> 111

<211> 283

<212> PRT

<213> Homo sapiens

<400> 111

Met Gly Leu Gly Leu Arg Gly Trp Gly Arg Pro Leu Leu Thr Val  
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Ala Thr Ala Leu Met Leu Pro Val Lys Pro Pro Ala Gly Ser Trp  
20 25 30

Gly Ala Gln Ile Ile Gly Gly His Glu Val Thr Pro His Ser Arg  
35 40 45

Pro Tyr Met Ala Ser Val Arg Phe Gly Gly Gln His His Cys Gly  
50 55 60

Gly Phe Leu Leu Arg Ala Arg Trp Val Val Ser Ala Ala His Cys  
65 70 75

Phe Ser His Arg Asp Leu Arg Thr Gly Leu Val Val Leu Gly Ala  
80 85 90

His Val Leu Ser Thr Ala Glu Pro Thr Gln Gln Val Phe Gly Ile  
95 100 105

Asp Ala Leu Thr Thr His Pro Asp Tyr His Pro Met Thr His Ala  
110 115 120

Asn Asp Ile Cys Leu Leu Arg Leu Asn Gly Ser Ala Val Leu Gly  
125 130 135

Pro Ala Val Gly Leu Leu Arg Leu Pro Gly Arg Arg Ala Arg Pro  
140 145 150

Pro Thr Ala Gly Thr Arg Cys Arg Val Ala Gly Trp Gly Phe Val  
155 160 165

Ser Asp Phe Glu Glu Leu Pro Pro Gly Leu Met Glu Ala Lys Val  
170 175 180

Arg Val Leu Asp Pro Asp Val Cys Asn Ser Ser Trp Lys Gly His  
185 190 195

Leu Thr Leu Thr Met Leu Cys Thr Arg Ser Gly Asp Ser His Arg  
200 205 210

Arg Gly Phe Cys Ser Ala Asp Ser Gly Gly Pro Leu Val Cys Arg  
215 220 225

Asn Arg Ala His Gly Leu Val Ser Phe Ser Gly Leu Trp Cys Gly  
230 235 240

Asp Pro Lys Thr Pro Asp Val Tyr Thr Gln Val Ser Ala Phe Val  
245 250 255

Ala Trp Ile Trp Asp Val Val Arg Arg Ser Ser Pro Gln Pro Gly  
 260 265 270

Pro Leu Pro Gly Thr Thr Arg Pro Pro Gly Glu Ala Ala  
 275 280

<210> 112  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 112  
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<210> 113  
 <211> 23  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-23  
 <223> Synthetic construct.

<400> 113  
 cgagaaggaa acgaggccgt gag 23

<210> 114  
 <211> 44  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-44  
 <223> Synthetic construct.

<400> 114  
 tgacacttac catgctctgc acccgcagtg gggacagcca caga 44

<210> 115  
 <211> 1808  
 <212> DNA  
 <213> Homo sapiens

<400> 115  
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 cctgacgcct gacgcctgtc cccggcccg catgagccgc tacctgctgc 100  
 cgctgtcggc gctgggcacg gtagcaggcg ccgccgtgct gctcaaggac 150  
 tatgtcaccg gtggggcttg cccagcaag gccaccatcc ctgggaagac 200



ggatcatcgtg	acgggacgcca	acacaggcat	cggaagcag	accgccttgg	250
aactggccag	gagaggaggc	aacatcatcc	tggcctgccg	agacatggag	300
aagtgtgagg	cggcagcaaa	ggacatccgc	ggggagaccc	tcaatcacca	350
tgtcaacgcc	cggcacctgg	acttggcttc	cctcaagtct	atccgagagt	400
ttgcagcaaa	gatcattgaa	gaggaggagc	gagtggacat	tctaataaac	450
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tgctggacaa	gctgaaagcc	tcagcccctt	cgcgatcat	caacctctcg	600
tccctggccc	atgttgctgg	gcacatagac	tttgacgact	tgaactggca	650
gacgaggaag	tataacacca	aagccgccta	ctgccagagc	aagctcgcca	700
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cacgggcatac	catggctoca	ccttctccag	caccacactc	gggcccattc	850
tctggctgct	ggtcaagagc	cccagagctg	ccgccagcc	cagcacatac	900
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gcctgtcggg	gagggttcca	aggtgctccg	tgaagagcat	gggcaagttg	1450
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gtcctctctg	agccttggtt	tcttcagcag	tgagatgctc	agaataactg	1550
ctgtctccca	tgatggtgtg	gtacagcgag	ctgttgctg	gctatggcat	1600
ggctgtgccg	ggggtgtttg	ctgagggtt	cctgtgccag	agcccagcca	1650

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 tgggaacccc accagctgct gctacaggac ctgggattgc ctgggactcc 1750  
 caccttctta tcaattctca tggtagtcca aactgcagac tctcaaactt 1800  
 gctcattt 1808

<210> 116  
 <211> 331  
 <212> PRT  
 <213> Homo sapiens

<400> 116  
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 Gly Ala Ala Val Leu Leu Lys Asp Tyr Val Thr Gly Gly Ala Cys  
 20 25 30  
 Pro Ser Lys Ala Thr Ile Pro Gly Lys Thr Val Ile Val Thr Gly  
 35 40 45  
 Ala Asn Thr Gly Ile Gly Lys Gln Thr Ala Leu Glu Leu Ala Arg  
 50 55 60  
 Arg Gly Gly Asn Ile Ile Leu Ala Cys Arg Asp Met Glu Lys Cys  
 65 70 75  
 Glu Ala Ala Ala Lys Asp Ile Arg Gly Glu Thr Leu Asn His His  
 80 85 90  
 Val Asn Ala Arg His Leu Asp Leu Ala Ser Leu Lys Ser Ile Arg  
 95 100 105  
 Glu Phe Ala Ala Lys Ile Ile Glu Glu Glu Glu Arg Val Asp Ile  
 110 115 120  
 Leu Ile Asn Asn Ala Gly Val Met Arg Cys Pro His Trp Thr Thr  
 125 130 135  
 Glu Asp Gly Phe Glu Met Gln Phe Gly Val Asn His Leu Gly His  
 140 145 150  
 Phe Leu Leu Thr Asn Leu Leu Leu Asp Lys Leu Lys Ala Ser Ala  
 155 160 165  
 Pro Ser Arg Ile Ile Asn Leu Ser Ser Leu Ala His Val Ala Gly  
 170 175 180  
 His Ile Asp Phe Asp Asp Leu Asn Trp Gln Thr Arg Lys Tyr Asn  
 185 190 195  
 Thr Lys Ala Ala Tyr Cys Gln Ser Lys Leu Ala Ile Val Leu Phe  
 200 205 210  
 Thr Lys Glu Leu Ser Arg Arg Leu Gln Gly Ser Gly Val Thr Val  
 215 220 225



agatgccttg gatcacttgg cctttgctta tttccgggca ggaaatgttt 750  
 cgtgtgccct cagcctctct cgaggagtttc ttctctacag cccagataat 800  
 aagaggatgg ccaggaatgt cttgaaatat gaaaggctct tggcagagag 850  
 ccccaaccac gtggtagctg aggctgtcat ccagaggccc aatatacccc 900  
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 cagcccactc tctaccagat ccctagcctc tactgttctt atgagaccaa 1000  
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<210> 118

<211> 544

<212> PRT

<213> Homo sapiens

<400> 118

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				20					25					30

Phe	Ser	Ala	Leu	Thr	Ser	Val	Ala	Arg	Ala	Leu	Ala	Pro	Glu	Arg
				35					40					45

Arg	Leu	Leu	Gly	Leu	Leu	Arg	Arg	Tyr	Leu	Arg	Gly	Glu	Glu	Ala
				50					55					60

Arg	Leu	Arg	Asp	Leu	Thr	Arg	Phe	Tyr	Asp	Lys	Val	Leu	Ser	Leu
				65					70					75

His	Glu	Asp	Ser	Thr	Thr	Pro	Val	Ala	Asn	Pro	Leu	Leu	Ala	Phe
				80					85					90

Thr	Leu	Ile	Lys	Arg	Leu	Gln	Ser	Asp	Trp	Arg	Asn	Val	Val	His
				95					100					105

Ser	Leu	Glu	Ala	Ser	Glu	Asn	Ile	Arg	Ala	Leu	Lys	Asp	Gly	Tyr
				110					115					120

Glu	Lys	Val	Glu	Gln	Asp	Leu	Pro	Ala	Phe	Glu	Asp	Leu	Glu	Gly
				125					130					135

Ala	Ala	Arg	Ala	Leu	Met	Arg	Leu	Gln	Asp	Val	Tyr	Met	Leu	Asn
				140					145					150

Val	Lys	Gly	Leu	Ala	Arg	Gly	Val	Phe	Gln	Arg	Val	Thr	Gly	Ser
				155					160					165

Ala	Ile	Thr	Asp	Leu	Tyr	Ser	Pro	Lys	Arg	Leu	Phe	Ser	Leu	Thr
				170					175					180

Gly	Asp	Asp	Cys	Phe	Gln	Val	Gly	Lys	Val	Ala	Tyr	Asp	Met	Gly
				185					190					195

Asp	Tyr	Tyr	His	Ala	Ile	Pro	Trp	Leu	Glu	Glu	Ala	Val	Ser	Leu
				200					205					210

Phe	Arg	Gly	Ser	Tyr	Gly	Glu	Trp	Lys	Thr	Glu	Asp	Glu	Ala	Ser
				215					220					225

Leu	Glu	Asp	Ala	Leu	Asp	His	Leu	Ala	Phe	Ala	Tyr	Phe	Arg	Ala
				230					235					240

Gly	Asn	Val	Ser	Cys	Ala	Leu	Ser	Leu	Ser	Arg	Glu	Phe	Leu	Leu	
				245					250					255	
Tyr	Ser	Pro	Asp	Asn	Lys	Arg	Met	Ala	Arg	Asn	Val	Leu	Lys	Tyr	
				260					265					270	
Glu	Arg	Leu	Leu	Ala	Glu	Ser	Pro	Asn	His	Val	Val	Ala	Glu	Ala	
				275					280					285	
Val	Ile	Gln	Arg	Pro	Asn	Ile	Pro	His	Leu	Gln	Thr	Arg	Asp	Thr	
				290					295					300	
Tyr	Glu	Gly	Leu	Cys	Gln	Thr	Leu	Gly	Ser	Gln	Pro	Thr	Leu	Tyr	
				305					310					315	
Gln	Ile	Pro	Ser	Leu	Tyr	Cys	Ser	Tyr	Glu	Thr	Asn	Ser	Asn	Ala	
				320					325					330	
Tyr	Leu	Leu	Leu	Gln	Pro	Ile	Arg	Lys	Glu	Val	Ile	His	Leu	Glu	
				335					340					345	
Pro	Tyr	Ile	Ala	Leu	Tyr	His	Asp	Phe	Val	Ser	Asp	Ser	Glu	Ala	
				350					355					360	
Gln	Lys	Ile	Arg	Glu	Leu	Ala	Glu	Pro	Trp	Leu	Gln	Arg	Ser	Val	
				365					370					375	
Val	Ala	Ser	Gly	Glu	Lys	Gln	Leu	Gln	Val	Glu	Tyr	Arg	Ile	Ser	
				380					385					390	
Lys	Ser	Ala	Trp	Leu	Lys	Asp	Thr	Val	Asp	Pro	Lys	Leu	Val	Thr	
				395					400					405	
Leu	Asn	His	Arg	Ile	Ala	Ala	Leu	Thr	Gly	Leu	Asp	Val	Arg	Pro	
				410					415					420	
Pro	Tyr	Ala	Glu	Tyr	Leu	Gln	Val	Val	Asn	Tyr	Gly	Ile	Gly	Gly	
				425					430					435	
His	Tyr	Glu	Pro	His	Phe	Asp	His	Ala	Thr	Ser	Pro	Ser	Ser	Pro	
				440					445					450	
Leu	Tyr	Arg	Met	Lys	Ser	Gly	Asn	Arg	Val	Ala	Thr	Phe	Met	Ile	
				455					460					465	
Tyr	Leu	Ser	Ser	Val	Glu	Ala	Gly	Gly	Ala	Thr	Ala	Phe	Ile	Tyr	
				470					475					480	
Ala	Asn	Leu	Ser	Val	Pro	Val	Val	Arg	Asn	Ala	Ala	Leu	Phe	Trp	
				485					490					495	
Trp	Asn	Leu	His	Arg	Ser	Gly	Glu	Gly	Asp	Ser	Asp	Thr	Leu	His	
				500					505					510	
Ala	Gly	Cys	Pro	Val	Leu	Val	Gly	Asp	Lys	Trp	Val	Ala	Asn	Lys	
				515					520					525	
Trp	Ile	His	Glu	Tyr	Gly	Gln	Glu	Phe	Arg	Arg	Pro	Cys	Ser	Ser	

530

535

540

Ser Pro Glu Asp

&lt;210&gt; 119

&lt;211&gt; 23

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;221&gt; Artificial Sequence

&lt;222&gt; 1-23

&lt;223&gt; Synthetic construct.

&lt;400&gt; 119

cgggacagga gacccagaaa ggg 23

&lt;210&gt; 120

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;221&gt; Artificial Sequence

&lt;222&gt; 1-24

&lt;223&gt; Synthetic construct.

&lt;400&gt; 120

ggccaagtga tccaaggcat cttc 24

&lt;210&gt; 121

&lt;211&gt; 49

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;221&gt; Artificial Sequence

&lt;222&gt; 1-49

&lt;223&gt; Synthetic construct.

&lt;400&gt; 121

ctgcgggacc tgactagatt ctacgacaag gtactttctt tgcattggg 49

&lt;210&gt; 122

&lt;211&gt; 1778

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 122

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gaatcggccc tggcaggtgg ggccacgagc gctggctgag ggaccgagcc 150

ggagagcccc ggagcccccg taaccgcgcg ggggagcgcc caggatgccg 200

gcgcggggact	cggagcaggt	gcgcctactgc	gcgcgccttct	cctacctctg	250
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<210> 123  
<211> 294  
<212> PRT  
<213> Homo sapiens

<400> 123  
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Phe Trp Leu Ile Gly Ala Leu Val Leu Ser Val Gly Ile Tyr Ala  
35 40 45  
Glu Val Glu Arg Gln Lys Tyr Lys Thr Leu Glu Ser Ala Phe Leu  
50 55 60  
Ala Pro Ala Ile Ile Leu Ile Leu Leu Gly Val Val Met Phe Met  
65 70 75  
Val Ser Phe Ile Gly Val Leu Ala Ser Leu Arg Asp Asn Leu Tyr  
80 85 90  
Leu Leu Gln Ala Phe Met Tyr Ile Leu Gly Ile Cys Leu Ile Met  
95 100 105  
Glu Leu Ile Gly Gly Val Val Ala Leu Thr Phe Arg Asn Gln Thr  
110 115 120  
Ile Asp Phe Leu Asn Asp Asn Ile Arg Arg Gly Ile Glu Asn Tyr  
125 130 135  
Tyr Asp Asp Leu Asp Phe Lys Asn Ile Met Asp Phe Val Gln Lys  
140 145 150  
Lys Phe Lys Cys Cys Gly Gly Glu Asp Tyr Arg Asp Trp Ser Lys  
155 160 165  
Asn Gln Tyr His Asp Cys Ser Ala Pro Gly Pro Leu Ala Cys Gly  
170 175 180  
Val Pro Tyr Thr Cys Cys Ile Arg Asn Thr Thr Glu Val Val Asn  
185 190 195  
Thr Met Cys Gly Tyr Lys Thr Ile Asp Lys Glu Arg Phe Ser Val  
200 205 210  
Gln Asp Val Ile Tyr Val Arg Gly Cys Thr Asn Ala Val Ile Ile  
215 220 225  
Trp Phe Met Asp Asn Tyr Thr Ile Met Ala Cys Ile Leu Leu Gly

230	235	240
Ile Leu Leu Pro Gln Phe Leu Gly Val	Leu Leu Thr Leu Leu Tyr	
245	250	255
Ile Thr Arg Val Glu Asp Ile Ile Met	Glu His Ser Val Thr Asp	
260	265	270
Gly Leu Leu Gly Pro Gly Ala Lys Pro	Ser Val Glu Ala Ala Gly	
275	280	285
Thr Gly Cys Cys Leu Cys Tyr Pro Asn		
290		

<210> 124  
 <211> 25  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-25  
 <223> Synthetic construct.

<400> 124  
 atcatctatt ccaccgtgtt ctggc 25

<210> 125  
 <211> 25  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-25  
 <223> Synthetic construct.

<400> 125  
 gacagagtgc tccatgatga tgtcc 25

<210> 126  
 <211> 50  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-50  
 <223> Synthetic construct.

<400> 126  
 cctgtctgtg ggcattctatg cagaggttga gcggcagaaa tataaaaccc 50

<210> 127  
 <211> 1636  
 <212> DNA  
 <213> Homo sapiens

<400> 127

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cctctctgca atcaataaac acttgccctgt gaaaaa 1636

<210> 128  
<211> 484  
<212> PRT  
<213> Homo sapiens

<400> 128  
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Ala Thr Leu Ile Gln Ala Thr Leu Ser Pro Thr Ala Val Leu Ile  
20 25 30  
Leu Gly Pro Lys Val Ile Lys Glu Lys Leu Thr Gln Glu Leu Lys  
35 40 45  
Asp His Asn Ala Thr Ser Ile Leu Gln Gln Leu Pro Leu Leu Ser  
50 55 60  
Ala Met Arg Glu Lys Pro Ala Gly Gly Ile Pro Val Leu Gly Ser  
65 70 75  
Leu Val Asn Thr Val Leu Lys His Ile Ile Trp Leu Lys Val Ile  
80 85 90  
Thr Ala Asn Ile Leu Gln Leu Gln Val Lys Pro Ser Ala Asn Asp  
95 100 105  
Gln Glu Leu Leu Val Lys Ile Pro Leu Asp Met Val Ala Gly Phe  
110 115 120  
Asn Thr Pro Leu Val Lys Thr Ile Val Glu Phe His Met Thr Thr  
125 130 135  
Glu Ala Gln Ala Thr Ile Arg Met Asp Thr Ser Ala Ser Gly Pro  
140 145 150  
Thr Arg Leu Val Leu Ser Asp Cys Ala Thr Ser His Gly Ser Leu  
155 160 165  
Arg Ile Gln Leu Leu Tyr Lys Leu Ser Phe Leu Val Asn Ala Leu  
170 175 180  
Ala Lys Gln Val Met Asn Leu Leu Val Pro Ser Leu Pro Asn Leu  
185 190 195  
Val Lys Asn Gln Leu Cys Pro Val Ile Glu Ala Ser Phe Asn Gly  
200 205 210  
Met Tyr Ala Asp Leu Leu Gln Leu Val Lys Val Pro Ile Ser Leu  
215 220 225

Ser	Ile	Asp	Arg	Leu	Glu	Phe	Asp	Leu	Leu	Tyr	Pro	Ala	Ile	Lys
				230					235					240
Gly	Asp	Thr	Ile	Gln	Leu	Tyr	Leu	Gly	Ala	Lys	Leu	Leu	Asp	Ser
				245					250					255
Gln	Gly	Lys	Val	Thr	Lys	Trp	Phe	Asn	Asn	Ser	Ala	Ala	Ser	Leu
				260					265					270
Thr	Met	Pro	Thr	Leu	Asp	Asn	Ile	Pro	Phe	Ser	Leu	Ile	Val	Ser
				275					280					285
Gln	Asp	Val	Val	Lys	Ala	Ala	Val	Ala	Ala	Val	Leu	Ser	Pro	Glu
				290					295					300
Glu	Phe	Met	Val	Leu	Leu	Asp	Ser	Val	Leu	Pro	Glu	Ser	Ala	His
				305					310					315
Arg	Leu	Lys	Ser	Ser	Ile	Gly	Leu	Ile	Asn	Glu	Lys	Ala	Ala	Asp
				320					325					330
Lys	Leu	Gly	Ser	Thr	Gln	Ile	Val	Lys	Ile	Leu	Thr	Gln	Asp	Thr
				335					340					345
Pro	Glu	Phe	Phe	Ile	Asp	Gln	Gly	His	Ala	Lys	Val	Ala	Gln	Leu
				350					355					360
Ile	Val	Leu	Glu	Val	Phe	Pro	Ser	Ser	Glu	Ala	Leu	Arg	Pro	Leu
				365					370					375
Phe	Thr	Leu	Gly	Ile	Glu	Ala	Ser	Ser	Glu	Ala	Gln	Phe	Tyr	Thr
				380					385					390
Lys	Gly	Asp	Gln	Leu	Ile	Leu	Asn	Leu	Asn	Asn	Ile	Ser	Ser	Asp
				395					400					405
Arg	Ile	Gln	Leu	Met	Asn	Ser	Gly	Ile	Gly	Trp	Phe	Gln	Pro	Asp
				410					415					420
Val	Leu	Lys	Asn	Ile	Ile	Thr	Glu	Ile	Ile	His	Ser	Ile	Leu	Leu
				425					430					435
Pro	Asn	Gln	Asn	Gly	Lys	Leu	Arg	Ser	Gly	Val	Pro	Val	Ser	Leu
				440					445					450
Val	Lys	Ala	Leu	Gly	Phe	Glu	Ala	Ala	Glu	Ser	Ser	Leu	Thr	Lys
				455					460					465
Asp	Ala	Leu	Val	Leu	Thr	Pro	Ala	Ser	Leu	Trp	Lys	Pro	Ser	Ser
				470					475					480
Pro	Val	Ser	Gln											

<210> 129  
 <211> 2213  
 <212> DNA  
 <213> Homo sapiens

&lt;400&gt; 129

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 cctgaccagg tgttcccaca tatgcctgtt acagataact acattaggaa 1450



Tyr Ser Ser Ala Phe Thr Asn Arg Ile Phe Phe Ala Met Val Asp  
110 115 120

Phe Asp Glu Gly Ser Asp Val Phe Gln Met Leu Asn Met Asn Ser  
125 130 135

Ala Pro Thr Phe Ile Asn Phe Pro Ala Lys Gly Lys Pro Lys Arg  
140 145 150

Gly Asp Thr Tyr Glu Leu Gln Val Arg Gly Phe Ser Ala Glu Gln  
155 160 165

Ile Ala Arg Trp Ile Ala Asp Arg Thr Asp Val Asn Ile Arg Val  
170 175 180

Ile Arg Pro Pro Asn Tyr Ala Gly Pro Leu Met Leu Gly Leu Leu  
185 190 195

Leu Ala Val Ile Gly Gly Leu Val Tyr Leu Arg Arg Ser Asn Met  
200 205 210

Glu Phe Leu Phe Asn Lys Thr Gly Trp Ala Phe Ala Ala Leu Cys  
215 220 225

Phe Val Leu Ala Met Thr Ser Gly Gln Met Trp Asn His Ile Arg  
230 235 240

Gly Pro Pro Tyr Ala His Lys Asn Pro His Thr Gly His Val Asn  
245 250 255

Tyr Ile His Gly Ser Ser Gln Ala Gln Phe Val Ala Glu Thr His  
260 265 270

Ile Val Leu Leu Phe Asn Gly Gly Val Thr Leu Gly Met Val Leu  
275 280 285

Leu Cys Glu Ala Ala Thr Ser Asp Met Asp Ile Gly Lys Arg Lys  
290 295 300

Ile Met Cys Val Ala Gly Ile Gly Leu Val Val Leu Phe Phe Ser  
305 310 315

Trp Met Leu Ser Ile Phe Arg Ser Lys Tyr His Gly Tyr Pro Tyr  
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Ser Phe Leu Met Ser  
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<210> 131

<211> 2476

<212> DNA

<213> Homo sapiens

<400> 131

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<210> 132  
<211> 536  
<212> PRT  
<213> Homo sapiens

<400> 132  
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20 25 30  
Ala Pro Asn Val Val Leu Val Val Ser Asp Ser Phe Asp Gly Arg  
35 40 45  
Leu Thr Phe His Pro Gly Ser Gln Val Val Lys Leu Pro Phe Ile  
50 55 60  
Asn Phe Met Lys Thr Arg Gly Thr Ser Phe Leu Asn Ala Tyr Thr  
65 70 75





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<210> 134  
 <211> 230  
 <212> PRT  
 <213> Homo sapiens

<400> 134  
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 Lys Thr Ser Ser Tyr Val Gly Ala Ser Ile Val Thr Ala Val Gly  
 35 40 45  
 Phe Ser Lys Gly Leu Trp Met Glu Cys Ala Thr His Ser Thr Gly

Ile Thr Gln Cys Asp	Ile Tyr Ser Thr	Leu Leu Gly Leu Pro Ala
65	70	75
Asp Ile Gln Ala Ala	Gln Ala Met Met	Val Thr Ser Ser Ala Ile
80	85	90
Ser Ser Leu Ala Cys	Ile Ile Ser Val	Val Gly Met Arg Cys Thr
95	100	105
Val Phe Cys Gln Glu	Ser Arg Ala Lys	Asp Arg Val Ala Val Ala
110	115	120
Gly Gly Val Phe Phe	Ile Leu Gly Gly	Leu Leu Gly Phe Ile Pro
125	130	135
Val Ala Trp Asn Leu	His Gly Ile Leu	Arg Asp Phe Tyr Ser Pro
140	145	150
Leu Val Pro Asp Ser	Met Lys Phe Glu	Ile Gly Glu Ala Leu Tyr
155	160	165
Leu Gly Ile Ile Ser	Ser Leu Phe Ser	Leu Ile Ala Gly Ile Ile
170	175	180
Leu Cys Phe Ser Cys	Ser Ser Gln Arg	Asn Arg Ser Asn Tyr Tyr
185	190	195
Asp Ala Tyr Gln Ala	Gln Pro Leu Ala	Thr Arg Ser Ser Pro Arg
200	205	210
Pro Gly Gln Pro Pro	Lys Val Lys Ser	Glu Phe Asn Ser Tyr Ser
215	220	225
Leu Thr Gly Tyr Val		
230		

<210> 135  
 <211> 610  
 <212> DNA  
 <213> Homo sapiens

<400> 135  
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Ile Arg His His	His Ser Glu His Arg Val His Gly Ala Met Glu				
	155		160		165
Leu Gln Val Gln	Thr Gly Lys Asp Ala Pro Ser Asn Cys Val Val				
	170		175		180
Tyr Pro Ser Ser	Ser Gln Asp Ser Glu Asn Ile Thr Ala Ala Ala				
	185		190		195
Leu Ala Thr Gly	Ala Cys Ile Val Gly Ile Leu Cys Leu Pro Leu				
	200		205		210
Ile Leu Leu Leu	Val Tyr Lys Gln Arg Gln Ala Ala Ser Asn Arg				
	215		220		225
Arg Ala Gln Glu	Leu Val Arg Met Asp Ser Asn Ile Gln Gly Ile				
	230		235		240
Glu Asn Pro Gly	Phe Glu Ala Ser Pro Pro Ala Gln Gly Ile Pro				
	245		250		255
Glu Ala Lys Val	Arg His Pro Leu Ser Tyr Val Ala Gln Arg Gln				
	260		265		270
Pro Ser Glu Ser	Gly Arg His Leu Leu Ser Glu Pro Ser Thr Pro				
	275		280		285
Leu Ser Pro Pro	Gly Pro Gly Asp Val Phe Phe Pro Ser Leu Asp				
	290		295		300
Pro Val Pro Asp	Ser Pro Asn Phe Glu Val Ile				
	305		310		

<210> 141  
 <211> 1732  
 <212> DNA  
 <213> Homo sapiens

<400> 141  
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[illegible]

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<210> 143
<211> 693
<212> DNA
<213> Homo sapiens
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<211> 693

<212> DNA

<213> Homo sapiens

<400> 143

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ggcgccagcg ggaggtcacc gtgagaccgg acttgccctcc gtgggcgccg 400

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<211> 93

<213> Homo sapiens

Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala Met Leu Gly  
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Gly Glu Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu Gln  
35 40 45

Asp Pro Arg Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu  
50 55 60

Leu Ala Thr Leu Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala  
65 70 75

Trp Arg Lys Asn Trp Met Val Gly Gly Glu Gly Gly Ala Ser Gly  
80 85 90

Arg Ser Pro

<211> 1883

<213> Homo sapiens

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caggctgcc tggggcccag caccctctc ctcatttgt tcctttttgc 150

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agtagtcggc atgctgctga gctgcgggac ttcaagaaca agatgctgcc 300

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acaccatctc cgggagagtg gatcgtctgg agcgggaggt agactatctg 400

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[illegible]

<211> 406

<213> Homo sapiens

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Glu Arg Arg Leu Ala Ala Leu Glu Glu Arg Leu Ala Gln Cys Gln  
35 40 45

Asp Gln Ser Ser Arg His Ala Ala Glu Leu Arg Asp Phe Lys Asn  
50 55 60

Lys Met Leu Pro Leu Leu Glu Val Ala Glu Lys Glu Arg Glu Ala  
65 70 75

Leu Arg Thr Glu Ala Asp Thr Ile Ser Gly Arg Val Asp Arg Leu  
80 85 90

Glu Arg Glu Val Asp Tyr Leu Glu Thr Gln Asn Pro Ala Leu Pro  
95 100 105

Cys Val Glu Phe Asp Glu Lys Val Thr Gly Gly Pro Gly Thr Lys  
110 115 120

Gly Lys Gly Arg Arg Asn Glu Lys Tyr Asp Met Val Thr Asp Cys  
125 130 135

Gly Tyr Thr Ile Ser Gln Val Arg Ser Met Lys Ile Leu Lys Arg  
140 145 150

Phe Gly Gly Pro Ala Gly Leu Trp Thr Lys Asp Pro Leu Gly Gln  
155 160 165

Thr Glu Lys Ile Tyr Val Leu Asp Gly Thr Gln Asn Asp Thr Ala  
170 175 180

Phe Val Phe Pro Arg Leu Arg Asp Phe Thr Leu Ala Met Ala Ala  
185 190 195

Arg Lys Ala Ser Arg Val Arg Val Pro Phe Pro Trp Val Gly Thr  
200 205 210

Gly Gln Leu Val Tyr Gly Gly Phe Leu Tyr Phe Ala Arg Arg Pro  
215 220 225

Pro Gly Arg Pro Gly Gly Gly Gly Glu Met Glu Asn Thr Leu Gln  
230 235 240

Leu Ile Lys Phe His Leu Ala Asn Arg Thr Val Val Asp Ser Ser  
245 250 255

10006769.120501

Val Phe Pro Ala Glu Gly Leu Ile Pro Pro Tyr Gly Leu Thr Ala  
260 265 270  
Asp Thr Tyr Ile Asp Leu Val Ala Asp Glu Glu Gly Leu Trp Ala  
275 280 285  
Val Tyr Ala Thr Arg Glu Asp Asp Arg His Leu Cys Leu Ala Lys  
290 295 300  
Leu Asp Pro Gln Thr Leu Asp Thr Glu Gln Gln Trp Asp Thr Pro  
305 310 315  
Cys Pro Arg Glu Asn Ala Glu Ala Ala Phe Val Ile Cys Gly Thr  
320 325 330  
Leu Tyr Val Val Tyr Asn Thr Arg Pro Ala Ser Arg Ala Arg Ile  
335 340 345  
Gln Cys Ser Phe Asp Ala Ser Gly Thr Leu Thr Pro Glu Arg Ala  
350 355 360  
Ala Leu Pro Tyr Phe Pro Arg Arg Tyr Gly Ala His Ala Ser Leu  
365 370 375  
Arg Tyr Asn Pro Arg Glu Arg Gln Leu Tyr Ala Trp Asp Asp Gly  
380 385 390  
Tyr Gln Ile Val Tyr Lys Leu Glu Met Arg Lys Lys Glu Glu Glu  
395 400 405

Val

<210> 147  
<211> 2052  
<212> DNA  
<213> Homo sapiens

<400> 147  
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 ataggggtct tcctggacta tgagtgtggg accatctcct tcttcaacat 1450  
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 tgaggcccta cattgagtat ccgtcctata atgagcaaaa tggaactccc 1550  
 atagtcatct gccagtcac ccaggaatca gagaaagagg cctcttggca 1600  
 aagggcctct gcaatcccag agacaagcaa cagtgagtcc tcctcacagg 1650  
 caaccacgcc ctctctcccc aggggtgaaa tgtaggatga atcacatccc 1700  
 acattcttct ttagggatat taaggtctct ctcccagatc caaagtcccg 1750  
 cagcagccgg ccaagggtggc ttccagatga agggggactg gcctgtccac 1800  
 atgggagtca ggtgtcatgg ctgccctgag ctgggaggga agaaggctga 1850  
 cattacattt agtttgctct cactccatct ggctaagtga tcttgaaata 1900  
 ccacctctca ggtgaagaac cgtcaggaat tcccatctca caggctgtgg 1950

tgtagattaa gtagacaagg aatgtgaata atgcttagat cttattgatg 2000  
acagagtgta tcctaatggt ttgttcatta tattacactt tcagtaaaaa 2050  
aa 2052

<210> 148  
<211> 500  
<212> PRT  
<213> Homo sapiens

<400> 148

Met	Ala	Leu	Met	Leu	Ser	Leu	Val	Leu	Ser	Leu	Leu	Lys	Leu	Gly	1	5	10	15
Ser	Gly	Gln	Trp	Gln	Val	Phe	Gly	Pro	Asp	Lys	Pro	Val	Gln	Ala	20	25	30	
Leu	Val	Gly	Glu	Asp	Ala	Ala	Phe	Ser	Cys	Phe	Leu	Ser	Pro	Lys	35	40	45	
Thr	Asn	Ala	Glu	Ala	Met	Glu	Val	Arg	Phe	Phe	Arg	Gly	Gln	Phe	50	55	60	
Ser	Ser	Val	Val	His	Leu	Tyr	Arg	Asp	Gly	Lys	Asp	Gln	Pro	Phe	65	70	75	
Met	Gln	Met	Pro	Gln	Tyr	Gln	Gly	Arg	Thr	Lys	Leu	Val	Lys	Asp	80	85	90	
Ser	Ile	Ala	Glu	Gly	Arg	Ile	Ser	Leu	Arg	Leu	Glu	Asn	Ile	Thr	95	100	105	
Val	Leu	Asp	Ala	Gly	Leu	Tyr	Gly	Cys	Arg	Ile	Ser	Ser	Gln	Ser	110	115	120	
Tyr	Tyr	Gln	Lys	Ala	Ile	Trp	Glu	Leu	Gln	Val	Ser	Ala	Leu	Gly	125	130	135	
Ser	Val	Pro	Leu	Ile	Ser	Ile	Thr	Gly	Tyr	Val	Asp	Arg	Asp	Ile	140	145	150	
Gln	Leu	Leu	Cys	Gln	Ser	Ser	Gly	Trp	Phe	Pro	Arg	Pro	Thr	Ala	155	160	165	
Lys	Trp	Lys	Gly	Pro	Gln	Gly	Gln	Asp	Leu	Ser	Thr	Asp	Ser	Arg	170	175	180	
Thr	Asn	Arg	Asp	Met	His	Gly	Leu	Phe	Asp	Val	Glu	Ile	Ser	Leu	185	190	195	
Thr	Val	Gln	Glu	Asn	Ala	Gly	Ser	Ile	Ser	Cys	Ser	Met	Arg	His	200	205	210	
Ala	His	Leu	Ser	Arg	Glu	Val	Glu	Ser	Arg	Val	Gln	Ile	Gly	Asp	215	220	225	
Thr	Phe	Phe	Glu	Pro	Ile	Ser	Trp	His	Leu	Ala	Thr	Lys	Val	Leu				

	230		235		240
Gly Ile Leu Cys	Cys Gly Leu Phe Phe	Gly Ile Val Gly Leu Lys			
	245		250		255
Ile Phe Phe Ser	Lys Phe Gln Trp Lys	Ile Gln Ala Glu Leu Asp			
	260		265		270
Trp Arg Arg Lys	His Gly Gln Ala Glu	Leu Arg Asp Ala Arg Lys			
	275		280		285
His Ala Val Glu	Val Thr Leu Asp Pro	Glu Thr Ala His Pro Lys			
	290		295		300
Leu Cys Val Ser	Asp Leu Lys Thr Val	Thr His Arg Lys Ala Pro			
	305		310		315
Gln Glu Val Pro	His Ser Glu Lys Arg	Phe Thr Arg Lys Ser Val			
	320		325		330
Val Ala Ser Gln	Ser Phe Gln Ala Gly	Lys His Tyr Trp Glu Val			
	335		340		345
Asp Gly Gly His	Asn Lys Arg Trp Arg	Val Gly Val Cys Arg Asp			
	350		355		360
Asp Val Asp Arg	Arg Lys Glu Tyr Val	Thr Leu Ser Pro Asp His			
	365		370		375
Gly Tyr Trp Val	Leu Arg Leu Asn Gly	Glu His Leu Tyr Phe Thr			
	380		385		390
Leu Asn Pro Arg	Phe Ile Ser Val Phe	Pro Arg Thr Pro Pro Thr			
	395		400		405
Lys Ile Gly Val	Phe Leu Asp Tyr Glu	Cys Gly Thr Ile Ser Phe			
	410		415		420
Phe Asn Ile Asn	Asp Gln Ser Leu Ile	Tyr Thr Leu Thr Cys Arg			
	425		430		435
Phe Glu Gly Leu	Leu Arg Pro Tyr Ile	Glu Tyr Pro Ser Tyr Asn			
	440		445		450
Glu Gln Asn Gly	Thr Pro Ile Val Ile	Cys Pro Val Thr Gln Glu			
	455		460		465
Ser Glu Lys Glu	Ala Ser Trp Gln Arg	Ala Ser Ala Ile Pro Glu			
	470		475		480
Thr Ser Asn Ser	Glu Ser Ser Ser Gln	Ala Thr Thr Pro Phe Leu			
	485		490		495
Pro Arg Gly Glu	Met				
	500				

<210> 149

<211> 24

<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 149  
gcgtggtcca cctctacagg gacg 24

<210> 150  
<211> 23  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-23  
<223> Synthetic construct.

<400> 150  
ggaactgacc cagtgtgac acc 23

<210> 151  
<211> 45  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-45  
<223> Synthetic construct.

<400> 151  
gcagatgcca cagtatcaag gcaggacaaa actggtgaag gattc 45

<210> 152  
<211> 2294  
<212> DNA  
<213> Homo sapiens

<400> 152  
gcgatggtgc gcccgggtggc ggtggcgggcg gcggttgcgg aggcttcctt 50  
ggtcggattg caacgaggag aagatgactg accaaccgac tggctgaatg 100  
aatgaatggc ggagccgagc gcgccatgag gagcctgccg agcctggggcg 150  
gcctcgccct gttgtgctgc gccgcgcgcg ccgcgcgcgt cgcctcagcc 200  
gcctcggcgg ggaatgtcac cgggtggcggc ggggcccgcgg ggcaggtgga 250  
cgcgtcgccg ggccccgggt tgcggggcga gccagccac cccttccta 300  
gggcgacggc tcccacggcc caggccccga ggaccgggcc cccgcgcgcc 350  
accgtccacc gaccctggc tgcgacttct ccagcccagt ccccgagac 400







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<210> 154
<211> 24
<212> DNA
<213> Artificial
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<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

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<400> 154
aactgctctg  tggttggaag  cctg 24
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<210> 155
<211> 24
<212> DNA
<213> Artificial
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<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

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<400> 155
cagtcacatg gctgacagac ccac 24
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<210> 156
<211> 38
<212> DNA
<213> Artificial
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<220>  
<221> Artificial Sequence  
<222> 1-38  
<223> Synthetic construct.

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<400> 156
  aggttatcag gggcttcact gtgaaacctg caaagagg 38
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<210> 157  
 <211> 689  
 <212> DNA  
 <213> Homo sapiens

<400> 157  
 tgcggcgcag tgtagacctg ggaggatggg cggcctgctg ctggctgctt 50  
 ttctggcttt ggtctcgggtg cccagggccc aggccgtgtg gttgggaaga 100  
 ctggaccctg agcagcttct tgggccctgg tacgtgcttg cggaggcctc 150  
 ccgggaaaag ggctttgccg tggagaagga catgaagaac gtcgtggggg 200  
 tgggtgtgac cctcactcca gaaaacaacc tgcggacgct gtcctctcag 250  
 cacgggctgg gaggggtgtg ccagagtgtc atggacctga taaagcgaaa 300  
 ctccggatgg gtgtttgaga atccctcaat aggcgtgctg gagctctggg 350  
 tgctggccac caacttcaga gactatgccg tcattctcac tcagctggag 400  
 ttccggggacg agcccttcaa caccgtggag ctgtacagtc tgacggagac 450  
 agccagccag gaggccatgg ggctcttcac caagtggagc aggagcctgg 500  
 gcttcctgtc acagtagcag gccagctgc agaaggacct cacctgtgct 550  
 cacaagatcc ttctgtgagt gctgcgtccc cagtagggat ggcgccaca 600  
 gggctctgtg acctcggcca gtgtccaccc acctcgtca gcggctcccg 650  
 gggcccagca ccagctcaga ataaagcgat tccacagca 689

<210> 158  
 <211> 163  
 <212> PRT  
 <213> Homo sapiens

<400> 158  
 Met Gly Gly Leu Leu Leu Ala Ala Phe Leu Ala Leu Val Ser Val  
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 Pro Arg Ala Gln Ala Val Trp Leu Gly Arg Leu Asp Pro Glu Gln  
 20 25 30  
 Leu Leu Gly Pro Trp Tyr Val Leu Ala Val Ala Ser Arg Glu Lys  
 35 40 45  
 Gly Phe Ala Met Glu Lys Asp Met Lys Asn Val Val Gly Val Val  
 50 55 60  
 Val Thr Leu Thr Pro Glu Asn Asn Leu Arg Thr Leu Ser Ser Gln  
 65 70 75  
 His Gly Leu Gly Gly Cys Asp Gln Ser Val Met Asp Leu Ile Lys  
 80 85 90

Arg	Asn	Ser	Gly	Trp	Val	Phe	Glu	Asn	Pro	Ser	Ile	Gly	Val	Leu
			95						100					105
Glu	Leu	Trp	Val	Leu	Ala	Thr	Asn	Phe	Arg	Asp	Tyr	Ala	Ile	Ile
			110						115					120
Phe	Thr	Gln	Leu	Glu	Phe	Gly	Asp	Glu	Pro	Phe	Asn	Thr	Val	Glu
			125						130					135
Leu	Tyr	Ser	Leu	Thr	Glu	Thr	Ala	Ser	Gln	Glu	Ala	Met	Gly	Leu
			140						145					150
Phe	Thr	Lys	Trp	Ser	Arg	Ser	Leu	Gly	Phe	Leu	Ser	Gln		
			155						160					

<210> 159  
 <211> 1665  
 <212> DNA  
 <213> Homo sapiens

<400> 159  
 aacagacgtt ccctcgcggc cctggcacct ctaaccccag acatgctgct 50  
 gctgctgctg cccctgctct gggggaggga gagggcggaa ggacagacaa 100  
 gtaaactgct gacgatgcag agttccgtga cgggtgcagga aggctgtgt 150  
 gtccatgtgc cctgctcctt ctccataccc tcgcatggct ggatttacct 200  
 tggcccagta gttcatggct actggttccg ggaagggggc aatacagacc 250  
 aggatgctcc agtggccaca aacaaccag ctcgggcagt gtgggaggag 300  
 actcgggacc gattccacct ccttggggac ccacatacca agaattgcac 350  
 cctgagcatc agagatgcca gaagaagtga tgcggggaga tacttctttc 400  
 gtatggagaa aggaagtata aaatggaatt ataaacatca ccggctctct 450  
 gtgaatgtga cagccttgac ccacaggccc aacatcctca tcccaggcac 500  
 cctggagtcc ggctgcccc agaatctgac ctgctctgtg ccctgggcct 550  
 gtgagcaggg gacacccct atgatctcct ggataggac ctccgtgtcc 600  
 cccctggacc cctccaccac ccgctcctcg gtgctcacc tcatcccaca 650  
 gccccaggac catggcacca gcctcacctg tcaggtgacc ttccctgggg 700  
 ccagcgtgac cacgaacaag accgtccatc tcaacgtgtc ctacccgcct 750  
 cagaacttga ccatgactgt cttccaagga gacggcacag tatccacagt 800  
 cttgggaaat ggctcatctc tgtcactccc agagggccag tctctgcgcc 850  
 tggctctgtc agttgatgca gttgacagca atccccctgc caggctgagc 900  
 ctgagctgga gaggcctgac cctgtgcccc tcacagccct caaaccgggg 950

ggtgctggag ctgccttggg tgcacctgag ggatgcagct gaattcacct 1000  
 gcagagctca gaaccctctc ggctctcagc aggtctacct gaacgtctcc 1050  
 ctgcagagca aagccacatc aggagtgact caggggggtgg tcgggggagc 1100  
 tggagccaca gccctggtct tcctgtcctt ctgcgtcatc ttcgtttag 1150  
 tgaggctctg caggaagaaa tcggcaaggc cagcagcggg cgtgggagat 1200  
 acgggcatag aggatgcaaa cgctgtcagg ggttcagcct ctcaggggcc 1250  
 cctgactgaa ccttgggcag aagacagtcc cccagaccag cctccccag 1300  
 cttctgcccg ctctcagtg ggggaaggag agctccagta tgcattccctc 1350  
 agcttcacga tgggtgaagcc ttgggactcg cggggacagg aggccactga 1400  
 caccgagtac tcggagatca agatccacag atgagaaact gcagagactc 1450  
 accctgattg agggatcaca gccctccag gcaagggaga agtcagaggc 1500  
 tgattcttgt agaattaaca gccctcaacg tgatgagcta tgataaact 1550  
 atgaattatg tgcagagtga aaagcacaca ggcttttagag tcaaagtatc 1600  
 tcaaactga atccacactg tgccctccct tttatTTTTT taactaaaag 1650  
 acagacaaat tccta 1665

<210> 160  
 <211> 463  
 <212> PRT  
 <213> Homo sapiens

<400> 160  
 Met Leu Leu Leu Leu Leu Pro Leu Leu Trp Gly Arg Glu Arg Ala  
 1 5 10 15  
 Glu Gly Gln Thr Ser Lys Leu Leu Thr Met Gln Ser Ser Val Thr  
 20 25 30  
 Val Gln Glu Gly Leu Cys Val His Val Pro Cys Ser Phe Ser Tyr  
 35 40 45  
 Pro Ser His Gly Trp Ile Tyr Pro Gly Pro Val Val His Gly Tyr  
 50 55 60  
 Trp Phe Arg Glu Gly Ala Asn Thr Asp Gln Asp Ala Pro Val Ala  
 65 70 75  
 Thr Asn Asn Pro Ala Arg Ala Val Trp Glu Glu Thr Arg Asp Arg  
 80 85 90  
 Phe His Leu Leu Gly Asp Pro His Thr Lys Asn Cys Thr Leu Ser  
 95 100 105  
 Ile Arg Asp Ala Arg Arg Ser Asp Ala Gly Arg Tyr Phe Phe Arg

				110					115					120
Met	Glu	Lys	Gly	Ser 125	Ile	Lys	Trp	Asn	Tyr 130	Lys	His	His	Arg	Leu 135
Ser	Val	Asn	Val	Thr 140	Ala	Leu	Thr	His	Arg 145	Pro	Asn	Ile	Leu	Ile 150
Pro	Gly	Thr	Leu	Glu 155	Ser	Gly	Cys	Pro	Gln 160	Asn	Leu	Thr	Cys	Ser 165
Val	Pro	Trp	Ala	Cys 170	Glu	Gln	Gly	Thr	Pro 175	Pro	Met	Ile	Ser	Trp 180
Ile	Gly	Thr	Ser	Val 185	Ser	Pro	Leu	Asp	Pro 190	Ser	Thr	Thr	Arg	Ser 195
Ser	Val	Leu	Thr	Leu 200	Ile	Pro	Gln	Pro	Gln 205	Asp	His	Gly	Thr	Ser 210
Leu	Thr	Cys	Gln	Val 215	Thr	Phe	Pro	Gly	Ala 220	Ser	Val	Thr	Thr	Asn 225
Lys	Thr	Val	His	Leu 230	Asn	Val	Ser	Tyr	Pro 235	Pro	Gln	Asn	Leu	Thr 240
Met	Thr	Val	Phe	Gln 245	Gly	Asp	Gly	Thr	Val 250	Ser	Thr	Val	Leu	Gly 255
Asn	Gly	Ser	Ser	Leu 260	Ser	Leu	Pro	Glu	Gly 265	Gln	Ser	Leu	Arg	Leu 270
Val	Cys	Ala	Val	Asp 275	Ala	Val	Asp	Ser	Asn 280	Pro	Pro	Ala	Arg	Leu 285
Ser	Leu	Ser	Trp	Arg 290	Gly	Leu	Thr	Leu	Cys 295	Pro	Ser	Gln	Pro	Ser 300
Asn	Pro	Gly	Val	Leu 305	Glu	Leu	Pro	Trp	Val 310	His	Leu	Arg	Asp	Ala 315
Ala	Glu	Phe	Thr	Cys 320	Arg	Ala	Gln	Asn	Pro 325	Leu	Gly	Ser	Gln	Gln 330
Val	Tyr	Leu	Asn	Val 335	Ser	Leu	Gln	Ser	Lys 340	Ala	Thr	Ser	Gly	Val 345
Thr	Gln	Gly	Val	Val 350	Gly	Gly	Ala	Gly	Ala 355	Thr	Ala	Leu	Val	Phe 360
Leu	Ser	Phe	Cys	Val 365	Ile	Phe	Val	Val	Val 370	Arg	Ser	Cys	Arg	Lys 375
Lys	Ser	Ala	Arg	Pro 380	Ala	Ala	Gly	Val	Gly 385	Asp	Thr	Gly	Ile	Glu 390
Asp	Ala	Asn	Ala	Val 395	Arg	Gly	Ser	Ala	Ser 400	Gln	Gly	Pro	Leu	Thr 405





*(The page contains faint, illegible markings or bleed-through from the reverse side.)*





Val	Gly	Gly	Glu	Thr 20	Arg	Ile	Ile	Lys	Gly 25	Phe	Glu	Cys	Lys	Pro 30
His	Ser	Gln	Pro	Trp 35	Gln	Ala	Ala	Leu	Phe 40	Glu	Lys	Thr	Arg	Leu 45
Leu	Cys	Gly	Ala	Thr 50	Leu	Ile	Ala	Pro	Arg 55	Trp	Leu	Leu	Thr	Ala 60
Ala	His	Cys	Leu	Lys 65	Pro	Arg	Tyr	Ile	Val 70	His	Leu	Gly	Gln	His 75
Asn	Leu	Gln	Lys	Glu 80	Glu	Gly	Cys	Glu	Gln 85	Thr	Arg	Thr	Ala	Thr 90
Glu	Ser	Phe	Pro	His 95	Pro	Gly	Phe	Asn	Asn 100	Ser	Leu	Pro	Asn	Lys 105
Asp	His	Arg	Asn	Asp 110	Ile	Met	Leu	Val	Lys 115	Met	Ala	Ser	Pro	Val 120
Ser	Ile	Thr	Trp	Ala 125	Val	Arg	Pro	Leu	Thr 130	Leu	Ser	Ser	Arg	Cys 135
Val	Thr	Ala	Gly	Thr 140	Ser	Cys	Leu	Ile	Ser 145	Gly	Trp	Gly	Ser	Thr 150
Ser	Ser	Pro	Gln	Leu 155	Arg	Leu	Pro	His	Thr 160	Leu	Arg	Cys	Ala	Asn 165
Ile	Thr	Ile	Ile	Glu 170	His	Gln	Lys	Cys	Glu 175	Asn	Ala	Tyr	Pro	Gly 180
Asn	Ile	Thr	Asp	Thr 185	Met	Val	Cys	Ala	Ser 190	Val	Gln	Glu	Gly	Gly 195
Lys	Asp	Ser	Cys	Gln 200	Gly	Asp	Ser	Gly	Gly 205	Pro	Leu	Val	Cys	Asn 210
Gln	Ser	Leu	Gln	Gly 215	Ile	Ile	Ser	Trp	Gly 220	Gln	Asp	Pro	Cys	Ala 225
Ile	Thr	Arg	Lys	Pro 230	Gly	Val	Tyr	Thr	Lys 235	Val	Cys	Lys	Tyr	Val 240
Asp	Trp	Ile	Gln	Glu 245	Thr	Met	Lys	Asn	Asn 250					

<210> 171

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-25

<223> Synthetic construct.

<400> 171  
ggctgcggga ctggaagtca tcggg 25

<210> 172  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 172  
ctccaggcca tgaggattct gcag 24

<210> 173  
<211> 18  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-18  
<223> Synthetic construct.

<400> 173  
cctctggtct gtaaccag 18

<210> 174  
<211> 24  
<212> DNA  
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<220>  
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<223> Synthetic construct.

<400> 174  
tctgtgatgt tgccggggta ggcg 24

<210> 175  
<211> 25  
<212> DNA  
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<220>  
<221> Artificial Sequence  
<222> 1-25  
<223> Synthetic construct.

<400> 175  
cgtgtagaca ccaggctttc gggtg 25

<210> 176  
<211> 18  
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<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-18

<223> Synthetic construct.

<400> 176

cccttgatga tcctgggc 18

<210> 177

<211> 50

<212> DNA

<213> Artificial

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<221> Artificial Sequence

<222> 1-50

<223> Synthetic construct.

<400> 177

aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggcctt 50

<210> 178

<211> 43

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-43

<223> Synthetic construct.

<400> 178

gagagaccag gatcatcaag gggttogagt gcaagcctca ctc 43

<210> 179

<211> 907

<212> DNA

<213> Homo sapiens

<400> 179

gagcagtgtt ctgctggagc cgatgocaaa aaccatgcat ttcttattca 50

gattcattgt tttcttttat ctgtggggcc tttttactgc tcagagacaa 100

aagaaaagagg agagcaccga agaagtgaaa atagaagttt tgcacgtcc 150

agaaaactgc tctaagacaa gcaagaagg agacctacta aatgcccatt 200

atgacggcta cctggctaaa gacggctcga aattctactg cagccggaca 250

caaaatgaag gccaccccaa atggtttgtt cttggtgttg ggcaagtcac 300

aaaaggccta gacattgcta tgacagatat gtgccctgga gaaaagcgaa 350

aagtagttat acccccttca tttgcatacg gaaaggaagg ctatgcagaa 400



Ile	Glu	Thr	Phe	Lys	Gln	Ile	Asp	Met	Asp	Asn	Asp	Arg	Gln	Leu
				155					160					165
Ser	Lys	Ala	Glu	Ile	Asn	Leu	Tyr	Leu	Gln	Arg	Glu	Phe	Glu	Lys
				170					175					180
Asp	Glu	Lys	Pro	Arg	Asp	Lys	Ser	Tyr	Gln	Asp	Ala	Val	Leu	Glu
				185					190					195
Asp	Ile	Phe	Lys	Lys	Asn	Asp	His	Asp	Gly	Asp	Gly	Phe	Ile	Ser
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Pro	Lys	Glu	Tyr	Asn	Val	Tyr	Gln	His	Asp	Glu	Leu			
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<210> 181  
 <211> 22  
 <212> DNA  
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 <221> Artificial Sequence  
 <222> 1-22  
 <223> Synthetic construct.  
  
 <400> 181  
 gtgttctgct ggagccgatg cc 22  
  
 <210> 182  
 <211> 18  
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 <222> 1-18  
 <223> Synthetic construct.  
  
 <400> 182  
 gacatggaca atgacagg 18  
  
 <210> 183  
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 <212> DNA  
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 <220>  
 <221> Artificial Sequence  
 <222> 1-18  
 <223> Synthetic construct.  
  
 <400> 183  
 cctttcagga tgtaggag 18  
  
 <210> 184  
 <211> 18  
 <212> DNA  
 <213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-18  
<223> Synthetic construct.

<400> 184  
gatgtctgcc accccaag 18

<210> 185  
<211> 27  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-27  
<223> Synthetic construct.

<400> 185  
gcatcctgat atgacttgct acgtggc 27

<210> 186  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 186  
tacaagaggg aagaggagtt gcac 24

<210> 187  
<211> 52  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-52  
<223> Synthetic construct.

<400> 187  
gccattatg acggctacct ggctaaagac ggctcgaaat tctactgcag 50  
cc 52

<210> 188  
<211> 573  
<212> DNA  
<213> Homo sapiens

<400> 188  
cagaaatgca gggaccattg cttcttccag gcctctgctt totgctgagc 50  
ctctttggag ctgtgactca gaaaaccaa acttcctgtg ctaagtgcc 100

cccaaagtct tcctgtgtca ataacactca ctgcacctgc aaccatggat 150  
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 aacgccaggc atggtggctc ggcctgttaa tcccagttct ttgggaagcc 250  
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 ggtgcatgcc tgcaatccca gttactcggg aggctgaggc aggagaatcg 400  
 cttgaactca ggaggcagaa gttgcagtga acccagatcc tgccattgca 450  
 ctccagcatg gatgacagag caagactccg tctcaaaaag aaaagatagt 500  
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 ccaaataaag tacttatatt ctc 573

<210> 189  
 <211> 74  
 <212> PRT  
 <213> Homo sapiens

<400> 189  
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 1 5 10 15  
 Leu Phe Gly Ala Val Thr Gln Lys Thr Lys Thr Ser Cys Ala Lys  
 20 25 30  
 Cys Pro Pro Asn Ala Ser Cys Val Asn Asn Thr His Cys Thr Cys  
 35 40 45  
 Asn His Gly Tyr Thr Ser Gly Ser Gly Gln Lys Leu Phe Thr Phe  
 50 55 60  
 Pro Leu Glu Thr Cys Asn Ala Arg His Gly Gly Ser Arg Leu  
 65 70

<210> 190  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 190  
 aggaccatt gcttcttcca ggcc 24

<210> 191  
 <211> 24  
 <212> DNA  
 <213> Artificial



<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 191  
cgttacatgt ctccaagggg aatg 24

<210> 192  
<211> 50  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-50  
<223> Synthetic construct.

<400> 192  
cctgtgctaa gtgccccca aatgcttct gtgtcaataa cactcactgc 50

<210> 193  
<211> 1091  
<212> DNA  
<213> Homo sapiens

<400> 193  
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gactttggaa gtgaccacc atgggggtca gcatcttttt gctcctgtgt 150  
gttcttgggc tcagccaggc agccacaccg aagattttca atggcactga 200  
gtgtgggcgt aactcacagc cgtggcaggt ggggctgttt gagggcacca 250  
gcctgcgctg cgggggtgtc cttattgacc acaggtgggt cctcacagcg 300  
gctcactgca gcggcagcag gtactgggtg cgctggggg aacacagcct 350  
cagccagctc gactggaccg agcagatccg gcacagcggc ttctctgtga 400  
cccatcccgg ctacctgga gcctcgacga gccacgagca cgacctccgg 450  
ctgctgcggc tgcgcctgcc cgtccgogta accagcagcg ttcaaccct 500  
gcccctgccc aatgactgtg caaccgctgg caccgagtgc cagctctcag 550  
gttggggcat caccaaccac ccacggaacc cattcccga tctgctccag 600  
tgcctcaacc tctccatcgt ctcccatgcc acctgccatg gtgtgtatcc 650  
cgggagaatc acgagcaaca tgggtgtgtgc aggcggcgtc ccggggcagg 700  
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caaggtctgg tgtcctgggg gtctgtgggg ccctgtggac aagatggcat 800

ccctggagtc tacacctata ttgtcaagta tgtggactgg atccggatga 850  
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 cttgggtacc cctctggccc tcagagcacc aatatctcct ccatcacttc 950  
 ccctagctcc actcttggtg gcctgggaac ttcttggaac tttaactcct 1000  
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 tggaataaat ataatgaag gaggggcaaa aaaaaaaaaa a 1091

<210> 194  
 <211> 248  
 <212> PRT  
 <213> Homo sapiens

<400> 194

Met	Gly	Leu	Ser	Ile	Phe	Leu	Leu	Leu	Cys	Val	Leu	Gly	Leu	Ser	1	5	10	15
Gln	Ala	Ala	Thr	Pro	Lys	Ile	Phe	Asn	Gly	Thr	Glu	Cys	Gly	Arg	20	25	30	
Asn	Ser	Gln	Pro	Trp	Gln	Val	Gly	Leu	Phe	Glu	Gly	Thr	Ser	Leu	35	40	45	
Arg	Cys	Gly	Gly	Val	Leu	Ile	Asp	His	Arg	Trp	Val	Leu	Thr	Ala	50	55	60	
Ala	His	Cys	Ser	Gly	Ser	Arg	Tyr	Trp	Val	Arg	Leu	Gly	Glu	His	65	70	75	
Ser	Leu	Ser	Gln	Leu	Asp	Trp	Thr	Glu	Gln	Ile	Arg	His	Ser	Gly	80	85	90	
Phe	Ser	Val	Thr	His	Pro	Gly	Tyr	Leu	Gly	Ala	Ser	Thr	Ser	His	95	100	105	
Glu	His	Asp	Leu	Arg	Leu	Leu	Arg	Leu	Arg	Leu	Pro	Val	Arg	Val	110	115	120	
Thr	Ser	Ser	Val	Gln	Pro	Leu	Pro	Leu	Pro	Asn	Asp	Cys	Ala	Thr	125	130	135	
Ala	Gly	Thr	Glu	Cys	His	Val	Ser	Gly	Trp	Gly	Ile	Thr	Asn	His	140	145	150	
Pro	Arg	Asn	Pro	Phe	Pro	Asp	Leu	Leu	Gln	Cys	Leu	Asn	Leu	Ser	155	160	165	
Ile	Val	Ser	His	Ala	Thr	Cys	His	Gly	Val	Tyr	Pro	Gly	Arg	Ile	170	175	180	
Thr	Ser	Asn	Met	Val	Cys	Ala	Gly	Gly	Val	Pro	Gly	Gln	Asp	Ala	185	190	195	
Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Gly	Gly	Val	Leu				



acccaggaca cagccactcg gggccccgct gccccagctg atccccactc 1100  
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 gcttggcatt gggagccctt caagaaggta ccagaaggaa ccctccagtc 1200  
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<210> 196  
 <211> 150  
 <212> PRT  
 <213> Homo sapiens

<400> 196  
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 Gly Leu Leu Lys Ala Arg Gln Glu Arg Arg Leu Ala Glu Ile Asn  
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 Arg Glu Phe Leu Cys Asp Gln Lys Tyr Ser Asp Glu Glu Asn Leu  
 35 40 45  
 Pro Glu Lys Leu Thr Ala Phe Lys Glu Lys Tyr Met Glu Phe Asp  
 50 55 60  
 Leu Asn Asn Glu Gly Glu Ile Asp Leu Met Ser Leu Lys Arg Met  
 65 70 75  
 Met Glu Lys Leu Gly Val Pro Lys Thr His Leu Glu Met Lys Lys  
 80 85 90  
 Met Ile Ser Glu Val Thr Gly Gly Val Ser Asp Thr Ile Ser Tyr  
 95 100 105  
 Arg Asp Phe Val Asn Met Met Leu Gly Lys Arg Ser Ala Val Leu  
 110 115 120  
 Lys Leu Val Met Met Phe Glu Gly Lys Ala Asn Glu Ser Ser Pro  
 125 130 135  
 Lys Pro Val Gly Pro Pro Pro Glu Arg Asp Ile Ala Ser Leu Pro  
 140 145 150

<210> 197  
 <211> 4842  
 <212> DNA  
 <213> Homo sapiens

<400> 197

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ggggtcggcg ccgcctgctg cgcctgcctg gcgctggcct tggcgtggc 150  
gagcgtcctg agtgggcctc cagccgtcgc ctgccccacc aagtgtacct 200  
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<210> 198

<211> 1523

<212> PRT

<213> Homo sapiens

<400> 198

Met	Ala	Pro	Gly	Trp	Ala	Gly	Val	Gly	Ala	Ala	Val	Arg	Ala	Arg	1	5	10	15
Leu	Ala	Leu	Ala	Leu	Ala	Leu	Ala	Ser	Val	Leu	Ser	Gly	Pro	Pro	20	25	30	
Ala	Val	Ala	Cys	Pro	Thr	Lys	Cys	Thr	Cys	Ser	Ala	Ala	Ser	Val	35	40	45	
Asp	Cys	His	Gly	Leu	Gly	Leu	Arg	Ala	Val	Pro	Arg	Gly	Ile	Pro	50	55	60	
Arg	Asn	Ala	Glu	Arg	Leu	Asp	Leu	Asp	Arg	Asn	Asn	Ile	Thr	Arg	65	70	75	
Ile	Thr	Lys	Met	Asp	Phe	Ala	Gly	Leu	Lys	Asn	Leu	Arg	Val	Leu	80	85	90	
His	Leu	Glu	Asp	Asn	Gln	Val	Ser	Val	Ile	Glu	Arg	Gly	Ala	Phe	95	100	105	
Gln	Asp	Leu	Lys	Gln	Leu	Glu	Arg	Leu	Arg	Leu	Asn	Lys	Asn	Lys	110	115	120	
Leu	Gln	Val	Leu	Pro	Glu	Leu	Leu	Phe	Gln	Ser	Thr	Pro	Lys	Leu	125	130	135	
Thr	Arg	Leu	Asp	Leu	Ser	Glu	Asn	Gln	Ile	Gln	Gly	Ile	Pro	Arg	140	145	150	
Lys	Ala	Phe	Arg	Gly	Ile	Thr	Asp	Val	Lys	Asn	Leu	Gln	Leu	Asp	155	160	165	



Asn Asn His Ile Ser Cys Ile Glu Asp Gly Ala Phe Arg Ala Leu	170	175	180
Arg Asp Leu Glu Ile Leu Thr Leu Asn Asn Asn Asn Ile Ser Arg	185	190	195
Ile Leu Val Thr Ser Phe Asn His Met Pro Lys Ile Arg Thr Leu	200	205	210
Arg Leu His Ser Asn His Leu Tyr Cys Asp Cys His Leu Ala Trp	215	220	225
Leu Ser Asp Trp Leu Arg Gln Arg Arg Thr Val Gly Gln Phe Thr	230	235	240
Leu Cys Met Ala Pro Val His Leu Arg Gly Phe Asn Val Ala Asp	245	250	255
Val Gln Lys Lys Glu Tyr Val Cys Pro Ala Pro His Ser Glu Pro	260	265	270
Pro Ser Cys Asn Ala Asn Ser Ile Ser Cys Pro Ser Pro Cys Thr	275	280	285
Cys Ser Asn Asn Ile Val Asp Cys Arg Gly Lys Gly Leu Met Glu	290	295	300
Ile Pro Ala Asn Leu Pro Glu Gly Ile Val Glu Ile Arg Leu Glu	305	310	315
Gln Asn Ser Ile Lys Ala Ile Pro Ala Gly Ala Phe Thr Gln Tyr	320	325	330
Lys Lys Leu Lys Arg Ile Asp Ile Ser Lys Asn Gln Ile Ser Asp	335	340	345
Ile Ala Pro Asp Ala Phe Gln Gly Leu Lys Ser Leu Thr Ser Leu	350	355	360
Val Leu Tyr Gly Asn Lys Ile Thr Glu Ile Ala Lys Gly Leu Phe	365	370	375
Asp Gly Leu Val Ser Leu Gln Leu Leu Leu Leu Asn Ala Asn Lys	380	385	390
Ile Asn Cys Leu Arg Val Asn Thr Phe Gln Asp Leu Gln Asn Leu	395	400	405
Asn Leu Leu Ser Leu Tyr Asp Asn Lys Leu Gln Thr Ile Ser Lys	410	415	420
Gly Leu Phe Ala Pro Leu Gln Ser Ile Gln Thr Leu His Leu Ala	425	430	435
Gln Asn Pro Phe Val Cys Asp Cys His Leu Lys Trp Leu Ala Asp	440	445	450
Tyr Leu Gln Asp Asn Pro Ile Glu Thr Ser Gly Ala Arg Cys Ser			

					455					460					465
Ser	Pro	Arg	Arg	Leu	Ala	Asn	Lys	Arg	Ile	Ser	Gln	Ile	Lys	Ser	
				470					475					480	
Lys	Lys	Phe	Arg	Cys	Ser	Gly	Ser	Glu	Asp	Tyr	Arg	Ser	Arg	Phe	
				485					490					495	
Ser	Ser	Glu	Cys	Phe	Met	Asp	Leu	Val	Cys	Pro	Glu	Lys	Cys	Arg	
				500					505					510	
Cys	Glu	Gly	Thr	Ile	Val	Asp	Cys	Ser	Asn	Gln	Lys	Leu	Val	Arg	
				515					520					525	
Ile	Pro	Ser	His	Leu	Pro	Glu	Tyr	Val	Thr	Asp	Leu	Arg	Leu	Asn	
				530					535					540	
Asp	Asn	Glu	Val	Ser	Val	Leu	Glu	Ala	Thr	Gly	Ile	Phe	Lys	Lys	
				545					550					555	
Leu	Pro	Asn	Leu	Arg	Lys	Ile	Asn	Leu	Ser	Asn	Asn	Lys	Ile	Lys	
				560					565					570	
Glu	Val	Arg	Glu	Gly	Ala	Phe	Asp	Gly	Ala	Ala	Ser	Val	Gln	Glu	
				575					580					585	
Leu	Met	Leu	Thr	Gly	Asn	Gln	Leu	Glu	Thr	Val	His	Gly	Arg	Val	
				590					595					600	
Phe	Arg	Gly	Leu	Ser	Gly	Leu	Lys	Thr	Leu	Met	Leu	Arg	Ser	Asn	
				605					610					615	
Leu	Ile	Ser	Cys	Val	Ser	Asn	Asp	Thr	Phe	Ala	Gly	Leu	Ser	Ser	
				620					625					630	
Val	Arg	Leu	Leu	Ser	Leu	Tyr	Asp	Asn	Arg	Ile	Thr	Thr	Ile	Thr	
				635					640					645	
Pro	Gly	Ala	Phe	Thr	Thr	Leu	Val	Ser	Leu	Ser	Thr	Ile	Asn	Leu	
				650					655					660	
Leu	Ser	Asn	Pro	Phe	Asn	Cys	Asn	Cys	His	Leu	Ala	Trp	Leu	Gly	
				665					670					675	
Lys	Trp	Leu	Arg	Lys	Arg	Arg	Ile	Val	Ser	Gly	Asn	Pro	Arg	Cys	
				680					685					690	
Gln	Lys	Pro	Phe	Phe	Leu	Lys	Glu	Ile	Pro	Ile	Gln	Asp	Val	Ala	
				695					700					705	
Ile	Gln	Asp	Phe	Thr	Cys	Asp	Gly	Asn	Glu	Glu	Ser	Ser	Cys	Gln	
				710					715					720	
Leu	Ser	Pro	Arg	Cys	Pro	Glu	Gln	Cys	Thr	Cys	Met	Glu	Thr	Val	
				725					730					735	
Val	Arg	Cys	Ser	Asn	Lys	Gly	Leu	Arg	Ala	Leu	Pro	Arg	Gly	Met	
				740					745					750	

Pro Lys Asp Val	Thr Glu Leu Tyr Leu	Glu Gly Asn His Leu	Thr
755		760	765
Ala Val Pro Arg	Glu Leu Ser Ala Leu	Arg His Leu Thr Leu	Ile
770		775	780
Asp Leu Ser Asn	Asn Ser Ile Ser Met	Leu Thr Asn Tyr Thr	Phe
785		790	795
Ser Asn Met Ser	His Leu Ser Thr Leu	Ile Leu Ser Tyr Asn	Arg
800		805	810
Leu Arg Cys Ile	Pro Val His Ala Phe	Asn Gly Leu Arg Ser	Leu
815		820	825
Arg Val Leu Thr	Leu His Gly Asn Asp	Ile Ser Ser Val Pro	Glu
830		835	840
Gly Ser Phe Asn	Asp Leu Thr Ser Leu	Ser His Leu Ala Leu	Gly
845		850	855
Thr Asn Pro Leu	His Cys Asp Cys Ser	Leu Arg Trp Leu Ser	Glu
860		865	870
Trp Val Lys Ala	Gly Tyr Lys Glu Pro	Gly Ile Ala Arg Cys	Ser
875		880	885
Ser Pro Glu Pro	Met Ala Asp Arg Leu	Leu Leu Thr Thr Pro	Thr
890		895	900
His Arg Phe Gln	Cys Lys Gly Pro Val	Asp Ile Asn Ile Val	Ala
905		910	915
Lys Cys Asn Ala	Cys Leu Ser Ser Pro	Cys Lys Asn Asn Gly	Thr
920		925	930
Cys Thr Gln Asp	Pro Val Glu Leu Tyr	Arg Cys Ala Cys Pro	Tyr
935		940	945
Ser Tyr Lys Gly	Lys Asp Cys Thr Val	Pro Ile Asn Thr Cys	Ile
950		955	960
Gln Asn Pro Cys	Gln His Gly Gly Thr	Cys His Leu Ser Asp	Ser
965		970	975
His Lys Asp Gly	Phe Ser Cys Ser Cys	Pro Leu Gly Phe Glu	Gly
980		985	990
Gln Arg Cys Glu	Ile Asn Pro Asp Asp	Cys Glu Asp Asn Asp	Cys
995		1000	1005
Glu Asn Asn Ala	Thr Cys Val Asp Gly	Ile Asn Asn Tyr Val	Cys
1010		1015	1020
Ile Cys Pro Pro	Asn Tyr Thr Gly Glu	Leu Cys Asp Glu Val	Ile
1025		1030	1035
Asp His Cys Val	Pro Glu Leu Asn Leu	Cys Gln His Glu Ala	Lys

				1040						1045					1050
Cys	Ile	Pro	Leu	Asp	Lys	Gly	Phe	Ser	Cys	Glu	Cys	Val	Pro	Gly	
				1055					1060					1065	
Tyr	Ser	Gly	Lys	Leu	Cys	Glu	Thr	Asp	Asn	Asp	Asp	Cys	Val	Ala	
				1070					1075					1080	
His	Lys	Cys	Arg	His	Gly	Ala	Gln	Cys	Val	Asp	Thr	Ile	Asn	Gly	
				1085					1090					1095	
Tyr	Thr	Cys	Thr	Cys	Pro	Gln	Gly	Phe	Ser	Gly	Pro	Phe	Cys	Glu	
				1100					1105					1110	
His	Pro	Pro	Pro	Met	Val	Leu	Leu	Gln	Thr	Ser	Pro	Cys	Asp	Gln	
				1115					1120					1125	
Tyr	Glu	Cys	Gln	Asn	Gly	Ala	Gln	Cys	Ile	Val	Val	Gln	Gln	Glu	
				1130					1135					1140	
Pro	Thr	Cys	Arg	Cys	Pro	Pro	Gly	Phe	Ala	Gly	Pro	Arg	Cys	Glu	
				1145					1150					1155	
Lys	Leu	Ile	Thr	Val	Asn	Phe	Val	Gly	Lys	Asp	Ser	Tyr	Val	Glu	
				1160					1165					1170	
Leu	Ala	Ser	Ala	Lys	Val	Arg	Pro	Gln	Ala	Asn	Ile	Ser	Leu	Gln	
				1175					1180					1185	
Val	Ala	Thr	Asp	Lys	Asp	Asn	Gly	Ile	Leu	Leu	Tyr	Lys	Gly	Asp	
				1190					1195					1200	
Asn	Asp	Pro	Leu	Ala	Leu	Glu	Leu	Tyr	Gln	Gly	His	Val	Arg	Leu	
				1205					1210					1215	
Val	Tyr	Asp	Ser	Leu	Ser	Ser	Pro	Pro	Thr	Thr	Val	Tyr	Ser	Val	
				1220					1225					1230	
Glu	Thr	Val	Asn	Asp	Gly	Gln	Phe	His	Ser	Val	Glu	Leu	Val	Thr	
				1235					1240					1245	
Leu	Asn	Gln	Thr	Leu	Asn	Leu	Val	Val	Asp	Lys	Gly	Thr	Pro	Lys	
				1250					1255					1260	
Ser	Leu	Gly	Lys	Leu	Gln	Lys	Gln	Pro	Ala	Val	Gly	Ile	Asn	Ser	
				1265					1270					1275	
Pro	Leu	Tyr	Leu	Gly	Gly	Ile	Pro	Thr	Ser	Thr	Gly	Leu	Ser	Ala	
				1280					1285					1290	
Leu	Arg	Gln	Gly	Thr	Asp	Arg	Pro	Leu	Gly	Gly	Phe	His	Gly	Cys	
				1295					1300					1305	
Ile	His	Glu	Val	Arg	Ile	Asn	Asn	Glu	Leu	Gln	Asp	Phe	Lys	Ala	
				1310					1315					1320	
Leu	Pro	Pro	Gln	Ser	Leu	Gly	Val	Ser	Pro	Gly	Cys	Lys	Ser	Cys	
				1325					1330					1335	



<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 200  
ttgttgcat tgaggaggag cagc 24

<210> 201  
<211> 50  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-50  
<223> Synthetic construct.

<400> 201  
gagggcatcg tcgaaatacg cctagaacag aactccatca aagccatccc 50

<210> 202  
<211> 753  
<212> DNA  
<213> Homo sapiens

<400> 202  
ggatgcagga cgctcccctg agctgcctgt caccgactag gtggagcagt 50  
gtttcttccg cagactcaac tgagaagtca gcctctgggg caggcaccag 100  
gaatctgcct tttcagttct gtctccggca ggctttgagg atgaaggctg 150  
cgggcattct gaccctcatt ggctgcctgg tcacaggcgc cgagtccaaa 200  
atctacactc gttgcaaact ggcaaaaata ttctcgaggg ctggcctgga 250  
caattactgg ggcttcagcc ttggaaactg gatctgcatg gcatattatg 300  
agagcggcta caacaccaca gcccgcagcg tcctggatga cggcagcatc 350  
gactatggca ttttccagat caacagcttc gcgtggtgca gacgcggaaa 400  
gctgaaggag aacaaccact gccatgtcgc ctgctcagcc ttgatcactg 450  
atgacctcac agatgcaatt atctgtgcca ggaaaattgt taaagagaca 500  
caaggaatga actattggca aggctggaag aaacattgtg agggcagaga 550  
cctgtccgag tggaaaaaag gctgtgaggt ttcttaaact ggaactggac 600  
ccaggatgct ttgcagcaac gccctaggat ttgcagtga tgtccaaatg 650  
cctgtgtcat cttgtcccgt ttctcccaa tttccttct caaacttga 700  
gagggaaaat taagctatac ttttaagaaa ataaatattt ccatttaa 750  
gtc 753

<210> 203  
 <211> 148  
 <212> PRT  
 <213> Homo sapiens

<400> 203

Met	Lys	Ala	Ala	Gly	Ile	Leu	Thr	Leu	Ile	Gly	Cys	Leu	Val	Thr
1				5					10					15
Gly	Ala	Glu	Ser	Lys	Ile	Tyr	Thr	Arg	Cys	Lys	Leu	Ala	Lys	Ile
				20					25					30
Phe	Ser	Arg	Ala	Gly	Leu	Asp	Asn	Tyr	Trp	Gly	Phe	Ser	Leu	Gly
				35					40					45
Asn	Trp	Ile	Cys	Met	Ala	Tyr	Tyr	Glu	Ser	Gly	Tyr	Asn	Thr	Thr
				50					55					60
Ala	Pro	Thr	Val	Leu	Asp	Asp	Gly	Ser	Ile	Asp	Tyr	Gly	Ile	Phe
				65					70					75
Gln	Ile	Asn	Ser	Phe	Ala	Trp	Cys	Arg	Arg	Gly	Lys	Leu	Lys	Glu
				80					85					90
Asn	Asn	His	Cys	His	Val	Ala	Cys	Ser	Ala	Leu	Ile	Thr	Asp	Asp
				95					100					105
Leu	Thr	Asp	Ala	Ile	Ile	Cys	Ala	Arg	Lys	Ile	Val	Lys	Glu	Thr
				110					115					120
Gln	Gly	Met	Asn	Tyr	Trp	Gln	Gly	Trp	Lys	Lys	His	Cys	Glu	Gly
				125					130					135
Arg	Asp	Leu	Ser	Glu	Trp	Lys	Lys	Gly	Cys	Glu	Val	Ser		
				140					145					

<210> 204  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 204  
 gcaggctttg aggatgaagg ctgc 24

<210> 205  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 205  
ctcattggct gcctggtcac aggc 24

<210> 206  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 206  
ccagtcggac aggtctctcc cctc 24

<210> 207  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 207  
tcagtgaacca aggctgagca ggcg 24

<210> 208  
<211> 47  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-47  
<223> Synthetic construct.

<400> 208  
ctacactcgt tgcaaactgg caaaaatatt ctcgagggct ggcctgg 47

<210> 209  
<211> 1648  
<212> DNA  
<213> Homo sapiens

<400> 209  
caggccatTT gcacccact gtccttTgtT tcggagccag gccacaccgt 50  
cctcagcagt gTcatgtgtT aaaaacgcca agctgaatat atcatgcccc 100  
tattaaaact tgtacatggc tccccattgg tttttggaga aaagttcaag 150  
ctttttacct tggTgtctgc ctgtatccca gtgttcaggc tggctagacg 200  
gcggaagaag atcctatTTT actgtcactt cccagatctg cttctcacca 250



agagagattc ttttcttaaa cgactataca gggccccaat tgactggata 300  
gaggaatata ccacagggcat ggcagactgc atcttagtca acagccagtt 350  
cacagctgct gttttttaagg aaacattcaa gtccctgtct cacatagacc 400  
ctgatgtcct ctatccatct ctaaagtgtca ccagctttga ctcagttggt 450  
cctgaaaagc tggatgacct agtccccaag gggaaaaaat tcctgctgct 500  
ctccatcaac agatacgaaa ggaagaaaaa tctgactttg gcaactggaag 550  
ccctagtaca gctgctgtga agattgacat cccaagattg ggagaggggt 600  
catctgatcg tggcaggtgg ttatgacgag agagtctctg agaattgtga 650  
acattatcag gaattgaaga aaatgggtcca acagtccgac cttggccagt 700  
atgtgacctt cttgaggtct ttctcagaca aacagaaaat ctccctcctc 750  
cacagctgca cgtgtgtgct ttacacacca agcaatgagc actttggcat 800  
tgtccctctg gaagccatgt acatgcagtg ccagtcatt gctgttaatt 850  
cgggtggacc cttggagtcc attgaccaca gtgtcacagg gtttctgtgt 900  
gagcctgacc cgggtgacct ctcagaagca atagaaaagt tcatccgtga 950  
accttcctta aaagccacca tgggcctggc tggaagagcc agagtgaagg 1000  
aaaaattttc ccctgaagca ttacagaaac agctctaccg atatgttacc 1050  
aaactgctgg tataatcaga ttgtttttaa gatctccatt aatgtcattt 1100  
ttatggattg tagaccaggt ttgaaacca aaaaagaaac ctagaatcta 1150  
atgcagaaga gatcttttaa aaaataaact tgagtcttga atgtgagcca 1200  
ctttcctata taccacacct ccctgtccac ttttcagaaa aaccatgtct 1250  
tttatgctat aatcattcca aattttgcca gtgttaagtt acaaattgtg 1300  
tgtcattcca tgttcagcag agtattttta ttatattttc tcgggattat 1350  
tgctcttctg tctataaatt ttgaatgata ctgtgcctta attggttttc 1400  
atagtttaag tgtgtatcat tatcaaagtt gattaatttg gttcatagt 1450  
ataatgagag cagggctatt gtagttccca gattcaatcc accgaagtgt 1500  
tcaactgcat ctgttaggga atttttgttt gtccctgtctt tgcctggatc 1550  
catagcgaga gtgctctgta ttttttttaa gataatttgt atttttgcac 1600  
actgagatat aataaaaggt gtttatcata aaaaaaaaaa aaaaaaaa 1648

<210> 210

<211> 323

<212> PRT

<213> Homo sapiens

<400> 210

Met	Pro	Leu	Leu	Lys	Leu	Val	His	Gly	Ser	Pro	Leu	Val	Phe	Gly
1				5					10					15
Glu	Lys	Phe	Lys	Leu	Phe	Thr	Leu	Val	Ser	Ala	Cys	Ile	Pro	Val
				20					25					30
Phe	Arg	Leu	Ala	Arg	Arg	Arg	Lys	Lys	Ile	Leu	Phe	Tyr	Cys	His
				35					40					45
Phe	Pro	Asp	Leu	Leu	Leu	Thr	Lys	Arg	Asp	Ser	Phe	Leu	Lys	Arg
				50					55					60
Leu	Tyr	Arg	Ala	Pro	Ile	Asp	Trp	Ile	Glu	Glu	Tyr	Thr	Thr	Gly
				65					70					75
Met	Ala	Asp	Cys	Ile	Leu	Val	Asn	Ser	Gln	Phe	Thr	Ala	Ala	Val
				80					85					90
Phe	Lys	Glu	Thr	Phe	Lys	Ser	Leu	Ser	His	Ile	Asp	Pro	Asp	Val
				95					100					105
Leu	Tyr	Pro	Ser	Leu	Asn	Val	Thr	Ser	Phe	Asp	Ser	Val	Val	Pro
				110					115					120
Glu	Lys	Leu	Asp	Asp	Leu	Val	Pro	Lys	Gly	Lys	Lys	Phe	Leu	Leu
				125					130					135
Leu	Ser	Ile	Asn	Arg	Tyr	Glu	Arg	Lys	Lys	Asn	Leu	Thr	Leu	Ala
				140					145					150
Leu	Glu	Ala	Leu	Val	Gln	Leu	Arg	Gly	Arg	Leu	Thr	Ser	Gln	Asp
				155					160					165
Trp	Glu	Arg	Val	His	Leu	Ile	Val	Ala	Gly	Gly	Tyr	Asp	Glu	Arg
				170					175					180
Val	Leu	Glu	Asn	Val	Glu	His	Tyr	Gln	Glu	Leu	Lys	Lys	Met	Val
				185					190					195
Gln	Gln	Ser	Asp	Leu	Gly	Gln	Tyr	Val	Thr	Phe	Leu	Arg	Ser	Phe
				200					205					210
Ser	Asp	Lys	Gln	Lys	Ile	Ser	Leu	Leu	His	Ser	Cys	Thr	Cys	Val
				215					220					225
Leu	Tyr	Thr	Pro	Ser	Asn	Glu	His	Phe	Gly	Ile	Val	Pro	Leu	Glu
				230					235					240
Ala	Met	Tyr	Met	Gln	Cys	Pro	Val	Ile	Ala	Val	Asn	Ser	Gly	Gly
				245					250					255
Pro	Leu	Glu	Ser	Ile	Asp	His	Ser	Val	Thr	Gly	Phe	Leu	Cys	Glu
				260					265					270

Pro Asp Pro Val His Phe Ser Glu Ala Ile Glu Lys Phe Ile Arg  
275 280 285

Glu Pro Ser Leu Lys Ala Thr Met Gly Leu Ala Gly Arg Ala Arg  
290 295 300

Val Lys Glu Lys Phe Ser Pro Glu Ala Phe Thr Glu Gln Leu Tyr  
305 310 315

Arg Tyr Val Thr Lys Leu Leu Val  
320

<210> 211

<211> 1554

<212> DNA

<213> Homo sapiens

<400> 211

gactacgccg atccgagacg tggctccctg ggccggcagaa ccatgttgga 50  
cttcgcgatc ttccgcttga ccttcttgct ggccgttggtg ggagccgtgc 100  
tctacctcta tccggcttcc agacaagctg caggaattcc agggattact 150  
ccaactgaag aaaaagatgg taatcttcca gatattgtga atagtgaag 200  
tttgcattgag ttccctggtta atttgcattga gagatatggg cctgtggtct 250  
ccttctggtt tggcaggcgc ctccgttggtta gtttgggcac tgttgatgta 300  
ctgaagcagc atatcaatcc caataagaca tcggaccctt ttgaaaccat 350  
gctgaagtca ttattaaggt atcaatctgg tgggtggcagt gtgagtgaag 400  
accacattgag gaaaaaattg tatgaaaatg gtgtgactga ttctctgaag 450  
agtaactttg ccctcctcct aaagctttca gaagaattat tagataaatg 500  
gctctcctac ccagagaccc agcacgtgcc cctcagccag catatgcttg 550  
gttttgctat gaagtctggt acacagattg taatgggtag tacatttgaa 600  
gatgatcagg aagtcattcg cttccagaag aatcatggca cagtttggtc 650  
tgagattgga aaaggctttc tagatgggtc acttgataaa aacatgactc 700  
ggaaaaaaca atatgaagat gccctcatgc aactggagtc tgttttaagg 750  
aacatcataa aagaacgaaa aggaaggaac ttcagtcaac atattttcat 800  
tgactcctta gtacaaggga accttaattga ccaacagatc ctagaagaca 850  
gtatgatatt ttctctggcc agttgcataa taactgcaaa attgtgtacc 900  
tgggcaatct gttttttaac cacctctgaa gaagttcaaa aaaaattata 950  
tgaagagata aaccaagttt ttggaaatgg tcctgttact ccagagaaaa 1000

ttgagcagct cagatattgt cagcatgtgc tttgtgaaac tggtcgaact 1050  
 gccaaactga ctccagtttc tgcccagctt caagatattg aaggaaaaat 1100  
 tgaccgattt attattccta gagagaccct cgtcctttat gcccttggtg 1150  
 tgggtacttca ggatcctaata acttggccat ctccacacaa gtttgatcca 1200  
 gatcggtttg atgatgaatt agtaatgaaa acttttttct cacttggatt 1250  
 ctcaggcaca caggagtgtc cagagttgag gtttgcatat atggtgacca 1300  
 cagtacttct tagtgtattg gtgaagagac tgcacctact ttctgtggag 1350  
 ggacagggtta ttgaaacaaa gtatgaactg gtaacatcat caagggaaga 1400  
 agcttggatc actgtctcaa agagatatta aaattttata catttaaaat 1450  
 cattgttaaa ttgattgagg aaaacaacca ttttaaaaaa atctatgttg 1500  
 aatcctttta taaaccagta tcactttgta atataaacac ctatttgtac 1550  
 ttaa 1554

<210> 212  
 <211> 462  
 <212> PRT  
 <213> Homo sapiens

<400> 212  
 Met Leu Asp Phe Ala Ile Phe Ala Val Thr Phe Leu Leu Ala Leu  
 1 5 10 15  
 Val Gly Ala Val Leu Tyr Leu Tyr Pro Ala Ser Arg Gln Ala Ala  
 20 25 30  
 Gly Ile Pro Gly Ile Thr Pro Thr Glu Glu Lys Asp Gly Asn Leu  
 35 40 45  
 Pro Asp Ile Val Asn Ser Gly Ser Leu His Glu Phe Leu Val Asn  
 50 55 60  
 Leu His Glu Arg Tyr Gly Pro Val Val Ser Phe Trp Phe Gly Arg  
 65 70 75  
 Arg Leu Val Val Ser Leu Gly Thr Val Asp Val Leu Lys Gln His  
 80 85 90  
 Ile Asn Pro Asn Lys Thr Ser Asp Pro Phe Glu Thr Met Leu Lys  
 95 100 105  
 Ser Leu Leu Arg Tyr Gln Ser Gly Gly Gly Ser Val Ser Glu Asn  
 110 115 120  
 His Met Arg Lys Lys Leu Tyr Glu Asn Gly Val Thr Asp Ser Leu  
 125 130 135  
 Lys Ser Asn Phe Ala Leu Leu Leu Lys Leu Ser Glu Glu Leu Leu

140	145	150
Asp Lys Trp Leu Ser Tyr Pro Glu Thr	Gln His Val Pro Leu Ser	
155	160	165
Gln His Met Leu Gly Phe Ala Met Lys	Ser Val Thr Gln Met Val	
170	175	180
Met Gly Ser Thr Phe Glu Asp Asp Gln	Glu Val Ile Arg Phe Gln	
185	190	195
Lys Asn His Gly Thr Val Trp Ser Glu	Ile Gly Lys Gly Phe Leu	
200	205	210
Asp Gly Ser Leu Asp Lys Asn Met Thr	Arg Lys Lys Gln Tyr Glu	
215	220	225
Asp Ala Leu Met Gln Leu Glu Ser Val	Leu Arg Asn Ile Ile Lys	
230	235	240
Glu Arg Lys Gly Arg Asn Phe Ser Gln	His Ile Phe Ile Asp Ser	
245	250	255
Leu Val Gln Gly Asn Leu Asn Asp Gln	Gln Ile Leu Glu Asp Ser	
260	265	270
Met Ile Phe Ser Leu Ala Ser Cys Ile	Ile Thr Ala Lys Leu Cys	
275	280	285
Thr Trp Ala Ile Cys Phe Leu Thr Thr	Ser Glu Glu Val Gln Lys	
290	295	300
Lys Leu Tyr Glu Glu Ile Asn Gln Val	Phe Gly Asn Gly Pro Val	
305	310	315
Thr Pro Glu Lys Ile Glu Gln Leu Arg	Tyr Cys Gln His Val Leu	
320	325	330
Cys Glu Thr Val Arg Thr Ala Lys Leu	Thr Pro Val Ser Ala Gln	
335	340	345
Leu Gln Asp Ile Glu Gly Lys Ile Asp	Arg Phe Ile Ile Pro Arg	
350	355	360
Glu Thr Leu Val Leu Tyr Ala Leu Gly	Val Val Leu Gln Asp Pro	
365	370	375
Asn Thr Trp Pro Ser Pro His Lys Phe	Asp Pro Asp Arg Phe Asp	
380	385	390
Asp Glu Leu Val Met Lys Thr Phe Ser	Ser Leu Gly Phe Ser Gly	
395	400	405
Thr Gln Glu Cys Pro Glu Leu Arg Phe	Ala Tyr Met Val Thr Thr	
410	415	420
Val Leu Leu Ser Val Leu Val Lys Arg	Leu His Leu Leu Ser Val	
425	430	435



Tyr Asp Lys Gln Asp Ile Gln Leu Val Ala Ala Leu Ser Val Thr  
 50 55 60  
 Leu Gly Leu Phe Ala Val Glu Leu Ala Gly Phe Leu Ser Gly Val  
 65 70 75  
 Ser Met Phe Asn Ser Thr Gln Ser Leu Ile Ser Ile Gly Ala His  
 80 85 90  
 Cys Ser Ala Ser Val Ala Leu Ser Phe Phe Ile Phe Glu Arg Trp  
 95 100 105  
 Glu Cys Thr Thr Tyr Trp Tyr Ile Phe Val Phe Cys Ser Ala Leu  
 110 115 120  
 Pro Ala Val Thr Glu Met Ala Leu Phe Val Thr Val Phe Gly Leu  
 125 130 135  
 Lys Lys Lys Pro Phe  
 140

<210> 215  
 <211> 697  
 <212> DNA  
 <213> Homo sapiens

<400> 215  
 tcccggaccc tgccgccctg ccactatgtc ccgccgctct atgctgcttg 50  
 cctgggctct cccagcctc cttcgactcg gagcggctca ggagacagaa 100  
 gacccggcct gctgcagccc catagtgcc cggaacgagt ggaaggccct 150  
 ggcatcagag tgcgcccagc acctgagcct gcccttacgc tatgtggtgg 200  
 tatcgcacac ggcgggcagc agctgcaaca ccccgccctc gtgccagcag 250  
 caggcccgga atgtgcagca ctaccacatg aagacactgg gctggtgcga 300  
 cgtgggctac aacttcctga ttggagaaga cgggctcgta tacgagggcc 350  
 gtggctggaa cttcacgggt gccactcag gtcacttatg gaaccccatg 400  
 tccattggca tcagcttcat gggcaactac atggatcggg tgcccacacc 450  
 ccaggccatc cgggcagccc agggctctact ggcctgcggt gtggctcagg 500  
 gagccctgag gtccaactat gtgctcaaag gacaccggga tgtgcagcgt 550  
 acactctctc caggcaacca gctctaccac ctcatccaga attggccaca 600  
 ctaccgctcc ccctgaggcc ctgctgatcc gcacccatt cctcccctcc 650  
 catggccaaa aacccactg tctccttctc caataaagat gtagctc 697

<210> 216  
 <211> 196  
 <212> PRT

<213> Homo sapiens

<400> 216

Met Ser Arg Arg Ser Met Leu Leu Ala Trp Ala Leu Pro Ser Leu  
1 5 10 15  
Leu Arg Leu Gly Ala Ala Gln Glu Thr Glu Asp Pro Ala Cys Cys  
20 25 30  
Ser Pro Ile Val Pro Arg Asn Glu Trp Lys Ala Leu Ala Ser Glu  
35 40 45  
Cys Ala Gln His Leu Ser Leu Pro Leu Arg Tyr Val Val Val Ser  
50 55 60  
His Thr Ala Gly Ser Ser Cys Asn Thr Pro Ala Ser Cys Gln Gln  
65 70 75  
Gln Ala Arg Asn Val Gln His Tyr His Met Lys Thr Leu Gly Trp  
80 85 90  
Cys Asp Val Gly Tyr Asn Phe Leu Ile Gly Glu Asp Gly Leu Val  
95 100 105  
Tyr Glu Gly Arg Gly Trp Asn Phe Thr Gly Ala His Ser Gly His  
110 115 120  
Leu Trp Asn Pro Met Ser Ile Gly Ile Ser Phe Met Gly Asn Tyr  
125 130 135  
Met Asp Arg Val Pro Thr Pro Gln Ala Ile Arg Ala Ala Gln Gly  
140 145 150  
Leu Leu Ala Cys Gly Val Ala Gln Gly Ala Leu Arg Ser Asn Tyr  
155 160 165  
Val Leu Lys Gly His Arg Asp Val Gln Arg Thr Leu Ser Pro Gly  
170 175 180  
Asn Gln Leu Tyr His Leu Ile Gln Asn Trp Pro His Tyr Arg Ser  
185 190 195  
Pro

<210> 217

<211> 1871

<212> DNA

<213> Homo sapiens

<400> 217

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<210> 218

<211> 252

<212> PRT

<213> Homo sapiens

<400> 218

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Glu	Asp	Pro	Glu	Arg	Asp	Asp	His	Glu	Gly	Gln	Pro	Arg	Pro	Arg	35	40	45	
Val	Pro	Arg	Lys	Arg	Gly	His	Ile	Ser	Pro	Lys	Ser	Arg	Pro	Met	50	55	60	
Ala	Asn	Ser	Thr	Leu	Leu	Gly	Leu	Leu	Ala	Pro	Pro	Gly	Glu	Ala	65	70	75	
Trp	Gly	Ile	Leu	Gly	Gln	Pro	Pro	Asn	Arg	Pro	Asn	His	Ser	Pro	80	85	90	
Pro	Pro	Ser	Ala	Lys	Val	Lys	Lys	Ile	Phe	Gly	Trp	Gly	Asp	Phe	95	100	105	
Tyr	Ser	Asn	Ile	Lys	Thr	Val	Ala	Leu	Asn	Leu	Leu	Val	Thr	Gly	110	115	120	
Lys	Ile	Val	Asp	His	Gly	Asn	Gly	Thr	Phe	Ser	Val	His	Phe	Gln	125	130	135	
His	Asn	Ala	Thr	Gly	Gln	Gly	Asn	Ile	Ser	Ile	Ser	Leu	Val	Pro	140	145	150	
Pro	Ser	Lys	Ala	Val	Glu	Phe	His	Gln	Glu	Gln	Gln	Ile	Phe	Ile	155	160	165	
Glu	Ala	Lys	Ala	Ser	Lys	Ile	Phe	Asn	Cys	Arg	Met	Glu	Trp	Glu	170	175	180	
Lys	Val	Glu	Arg	Gly	Arg	Arg	Thr	Ser	Leu	Cys	Thr	His	Asp	Pro	185	190	195	
Ala	Lys	Ile	Cys	Ser	Arg	Asp	His	Ala	Gln	Ser	Ser	Ala	Thr	Trp	200	205	210	

Ser Cys Ser Gln Pro Phe Lys Val Val Cys Val Tyr Ile Ala Phe  
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Tyr Ser Thr Asp Tyr Arg Leu Val Gln Lys Val Cys Pro Asp Tyr  
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Asn Tyr His Ser Asp Thr Pro Tyr Tyr Pro Ser Gly  
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<211> 2065

<212> DNA

<213> Homo sapiens

<400> 219

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<210> 220
<211> 201
<212> PRT
<213> Homo sapiens
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Leu Val Leu Thr Leu Pro Gly Leu Pro Val Trp Ala Gln Asn Asp
          20          25
Thr Glu Pro Ile Val Leu Glu Gly Lys Cys Leu Val Val Cys Asp
          35          40
Ser Asn Pro Ala Thr Asp Ser Lys Gly Ser Ser Ser Ser Pro Leu
          50          55          60

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Gly	Ile	Ser	Val	Arg	Ala	Ala	Asn	Ser	Lys	Val	Ala	Phe	Ser	Ala	
				65					70					75	
Val	Arg	Ser	Thr	Asn	His	Glu	Pro	Ser	Glu	Met	Ser	Asn	Lys	Thr	
				80					85					90	
Arg	Ile	Ile	Tyr	Phe	Asp	Gln	Ile	Leu	Val	Asn	Val	Gly	Asn	Phe	
				95					100					105	
Phe	Thr	Leu	Glu	Ser	Val	Phe	Val	Ala	Pro	Arg	Lys	Gly	Ile	Tyr	
				110					115					120	
Ser	Phe	Ser	Phe	His	Val	Ile	Lys	Val	Tyr	Gln	Ser	Gln	Thr	Ile	
				125					130					135	
Gln	Val	Asn	Leu	Met	Leu	Asn	Gly	Lys	Pro	Val	Ile	Ser	Ala	Phe	
				140					145					150	
Ala	Gly	Asp	Lys	Asp	Val	Thr	Arg	Glu	Ala	Ala	Thr	Asn	Gly	Val	
				155					160					165	
Leu	Leu	Tyr	Leu	Asp	Lys	Glu	Asp	Lys	Val	Tyr	Leu	Lys	Leu	Glu	
				170					175					180	
Lys	Gly	Asn	Leu	Val	Gly	Gly	Trp	Gln	Tyr	Ser	Thr	Phe	Ser	Gly	
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<210> 221  
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 <212> DNA  
 <213> Artificial  
  
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<210>	225
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<213> Homo sapiens

<400> 225

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Arg Ile Ile Phe Leu Ile Ala Gly Ala Phe Phe Trp Leu Val Ser  
35 40 45  
Leu Leu Ile Ser Ser Leu Val Trp Phe Met Ala Arg Val Ile Ile  
50 55 60  
Asp Asn Lys Asp Gly Pro Thr Gln Lys Tyr Leu Leu Ile Phe Gly  
65 70 75  
Ala Phe Val Ser Val Tyr Ile Gln Glu Met Phe Arg Phe Ala Tyr  
80 85 90  
Tyr Lys Leu Leu Lys Lys Ala Ser Glu Gly Leu Lys Ser Ile Asn  
95 100 105  
Pro Gly Glu Thr Ala Pro Ser Met Arg Leu Leu Ala Tyr Val Ser  
110 115 120  
Gly Leu Gly Phe Gly Ile Met Ser Gly Val Phe Ser Phe Val Asn  
125 130 135  
Thr Leu Ser Asp Ser Leu Gly Pro Gly Thr Val Gly Ile His Gly  
140 145 150  
Asp Ser Pro Gln Phe Phe Leu Tyr Ser Ala Phe Met Thr Leu Val  
155 160 165  
Ile Ile Leu Leu His Val Phe Trp Gly Ile Val Phe Phe Asp Gly  
170 175 180  
Cys Glu Lys Lys Lys Trp Gly Ile Leu Leu Ile Val Leu Leu Thr  
185 190 195  
His Leu Leu Val Ser Ala Gln Thr Phe Ile Ser Ser Tyr Tyr Gly  
200 205 210  
Ile Asn Leu Ala Ser Ala Phe Ile Ile Leu Val Leu Met Gly Thr  
215 220 225  
Trp Ala Phe Leu Ala Ala Gly Gly Ser Cys Arg Ser Leu Lys Leu  
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245 250 255  
Ser Arg

<210> 226

**THE**

210



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<211> 832

<212> PRT

<213> Homo sapiens

<400> 227

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Val	Glu	Ser	His	Leu	Gly	Val	Leu	Gly	Pro	Lys	Asn	Val	Ser	Gln
				20					25					30

10006768-100001

Lys	Asp	Ala	Glu	Phe	Glu	Arg	Thr	Tyr	Val	Asp	Glu	Val	Asn	Ser		35	40	45
Glu	Leu	Val	Asn	Ile	Tyr	Thr	Phe	Asn	His	Thr	Val	Thr	Arg	Asn		50	55	60
Arg	Thr	Glu	Gly	Val	Arg	Val	Ser	Val	Asn	Val	Leu	Asn	Lys	Gln		65	70	75
Lys	Gly	Ala	Pro	Leu	Leu	Phe	Val	Val	Arg	Gln	Lys	Glu	Ala	Val		80	85	90
Val	Ser	Phe	Gln	Val	Pro	Leu	Ile	Leu	Arg	Gly	Met	Phe	Gln	Arg		95	100	105
Lys	Tyr	Leu	Tyr	Gln	Lys	Val	Glu	Arg	Thr	Leu	Cys	Gln	Pro	Pro		110	115	120
Thr	Lys	Asn	Glu	Ser	Glu	Ile	Gln	Phe	Phe	Tyr	Val	Asp	Val	Ser		125	130	135
Thr	Leu	Ser	Pro	Val	Asn	Thr	Thr	Tyr	Gln	Leu	Arg	Val	Ser	Arg		140	145	150
Met	Asp	Asp	Phe	Val	Leu	Arg	Thr	Gly	Glu	Gln	Phe	Ser	Phe	Asn		155	160	165
Thr	Thr	Ala	Ala	Gln	Pro	Gln	Tyr	Phe	Lys	Tyr	Glu	Phe	Pro	Glu		170	175	180
Gly	Val	Asp	Ser	Val	Ile	Val	Lys	Val	Thr	Ser	Asn	Lys	Ala	Phe		185	190	195
Pro	Cys	Ser	Val	Ile	Ser	Ile	Gln	Asp	Val	Leu	Cys	Pro	Val	Tyr		200	205	210
Asp	Leu	Asp	Asn	Asn	Val	Ala	Phe	Ile	Gly	Met	Tyr	Gln	Thr	Met		215	220	225
Thr	Lys	Lys	Ala	Ala	Ile	Thr	Val	Gln	Arg	Lys	Asp	Phe	Pro	Ser		230	235	240
Asn	Ser	Phe	Tyr	Val	Val	Val	Val	Val	Lys	Thr	Glu	Asp	Gln	Ala		245	250	255
Cys	Gly	Gly	Ser	Leu	Pro	Phe	Tyr	Pro	Phe	Ala	Glu	Asp	Glu	Pro		260	265	270
Val	Asp	Gln	Gly	His	Arg	Gln	Lys	Thr	Leu	Ser	Val	Leu	Val	Ser		275	280	285
Gln	Ala	Val	Thr	Ser	Glu	Ala	Tyr	Val	Ser	Gly	Met	Leu	Phe	Cys		290	295	300
Leu	Gly	Ile	Phe	Leu	Ser	Phe	Tyr	Leu	Leu	Thr	Val	Leu	Leu	Ala		305	310	315
Cys	Trp	Glu	Asn	Trp	Arg	Gln	Lys	Lys	Lys	Thr	Leu	Leu	Val	Ala				

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Ile Asp Arg Ala Cys	335	Pro Glu Ser Gly His	340	Pro Arg Val Leu Ala	345
Asp Ser Phe Pro Gly	350	Ser Ser Pro Tyr Glu	355	Gly Tyr Asn Tyr Gly	360
Ser Phe Glu Asn Val	365	Ser Gly Ser Thr Asp	370	Gly Leu Val Asp Ser	375
Ala Gly Thr Gly Asp	380	Leu Ser Tyr Gly Tyr	385	Gln Gly Arg Ser Phe	390
Glu Pro Val Gly Thr	395	Arg Pro Arg Val Asp	400	Ser Met Ser Ser Val	405
Glu Glu Asp Asp Tyr	410	Asp Thr Leu Thr Asp	415	Ile Asp Ser Asp Lys	420
Asn Val Ile Arg Thr	425	Lys Gln Tyr Leu Tyr	430	Val Ala Asp Leu Ala	435
Arg Lys Asp Lys Arg	440	Val Leu Arg Lys Lys	445	Tyr Gln Ile Tyr Phe	450
Trp Asn Ile Ala Thr	455	Ile Ala Val Phe Tyr	460	Ala Leu Pro Val Val	465
Gln Leu Val Ile Thr	470	Tyr Gln Thr Val Val	475	Asn Val Thr Gly Asn	480
Gln Asp Ile Cys Tyr	485	Tyr Asn Phe Leu Cys	490	Ala His Pro Leu Gly	495
Asn Leu Ser Ala Phe	500	Asn Asn Ile Leu Ser	505	Asn Leu Gly Tyr Ile	510
Leu Leu Gly Leu Leu	515	Phe Leu Leu Ile Ile	520	Leu Gln Arg Glu Ile	525
Asn His Asn Arg Ala	530	Leu Leu Arg Asn Asp	535	Leu Cys Ala Leu Glu	540
Cys Gly Ile Pro Lys	545	His Phe Gly Leu Phe	550	Tyr Ala Met Gly Thr	555
Ala Leu Met Met Glu	560	Gly Leu Leu Ser Ala	565	Cys Tyr His Val Cys	570
Pro Asn Tyr Thr Asn	575	Phe Gln Phe Asp Thr	580	Ser Phe Met Tyr Met	585
Ile Ala Gly Leu Cys	590	Met Leu Lys Leu Tyr	595	Gln Lys Arg His Pro	600
Asp Ile Asn Ala Ser	605	Ala Tyr Ser Ala Tyr	610	Ala Cys Leu Ala Ile	615

10006758-10006759

Val Ile Phe Phe Ser Val Leu Gly Val Val Phe Gly Lys Gly Asn  
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Thr Ala Phe Trp Ile Val Phe Ser Ile Ile His Ile Ile Ala Thr  
635 640 645

Leu Leu Leu Ser Thr Gln Leu Tyr Tyr Met Gly Arg Trp Lys Leu  
650 655 660

Asp Ser Gly Ile Phe Arg Arg Ile Leu His Val Leu Tyr Thr Asp  
665 670 675

Cys Ile Arg Gln Cys Ser Gly Pro Leu Tyr Val Asp Arg Met Val  
680 685 690

Leu Leu Val Met Gly Asn Val Ile Asn Trp Ser Leu Ala Ala Tyr  
695 700 705

Gly Leu Ile Met Arg Pro Asn Asp Phe Ala Ser Tyr Leu Leu Ala  
710 715 720

Ile Gly Ile Cys Asn Leu Leu Leu Tyr Phe Ala Phe Tyr Ile Ile  
725 730 735

Met Lys Leu Arg Ser Gly Glu Arg Ile Lys Leu Ile Pro Leu Leu  
740 745 750

Cys Ile Val Cys Thr Ser Val Val Trp Gly Phe Ala Leu Phe Phe  
755 760 765

Phe Phe Gln Gly Leu Ser Thr Trp Gln Lys Thr Pro Ala Glu Ser  
770 775 780

Arg Glu His Asn Arg Asp Cys Ile Leu Leu Asp Phe Phe Asp Asp  
785 790 795

His Asp Ile Trp His Phe Leu Ser Ser Ile Ala Met Phe Gly Ser  
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815 820 825

Arg Asp Lys Ile Tyr Val Phe  
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<212> DNA  
<213> Homo sapiens

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<211> 807  
<212> PRT  
<213> Homo sapiens

<400> 229  
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Ser	Gly	Lys	Ala	Thr 65	Glu	Gly	Pro	Phe	Ala 70	Met	Asp	Pro	Asp	Ser 75
Gly	Phe	Leu	Leu	Val 80	Thr	Arg	Ala	Leu	Asp 85	Arg	Glu	Glu	Gln	Ala 90
Glu	Tyr	Gln	Leu	Gln 95	Val	Thr	Leu	Glu	Met 100	Gln	Asp	Gly	His	Val 105
Leu	Trp	Gly	Pro	Gln 110	Pro	Val	Leu	Val	His 115	Val	Lys	Asp	Glu	Asn 120
Asp	Gln	Val	Pro	His 125	Phe	Ser	Gln	Ala	Ile 130	Tyr	Arg	Ala	Arg	Leu 135
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Ser	Asp	Arg	Asp	Glu 155	Pro	Gly	Thr	Ala	Asn 160	Ser	Asp	Leu	Arg	Phe 165
His	Ile	Leu	Ser	Gln 170	Ala	Pro	Ala	Gln	Pro 175	Ser	Pro	Asp	Met	Phe 180
Gln	Leu	Glu	Pro	Arg 185	Leu	Gly	Ala	Leu	Ala 190	Leu	Ser	Pro	Lys	Gly 195
Ser	Thr	Ser	Leu	Asp 200	His	Ala	Leu	Glu	Arg 205	Thr	Tyr	Gln	Leu	Leu 210
Val	Gln	Val	Lys	Asp 215	Met	Gly	Asp	Gln	Ala 220	Ser	Gly	His	Gln	Ala 225
Thr	Ala	Thr	Val	Glu 230	Val	Ser	Ile	Ile	Glu 235	Ser	Thr	Trp	Val	Ser 240
Leu	Glu	Pro	Ile	His 245	Leu	Ala	Glu	Asn	Leu 250	Lys	Val	Leu	Tyr	Pro 255
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Gly	Asn	Leu	Tyr	Val 290	Thr	Arg	Glu	Leu	Asp 295	Arg	Glu	Ala	Gln	Ala 300
Glu	Tyr	Leu	Leu	Gln 305	Val	Arg	Ala	Gln	Asn 310	Ser	His	Gly	Glu	Asp 315





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Thr	Tyr	Thr	Val	Leu 635	Val	Glu	Ala	Gln	Asp 640	Thr	Ala	Leu	Thr	Leu 645
Ala	Pro	Val	Pro	Ser 650	Gln	Tyr	Leu	Cys	Thr 655	Pro	Arg	Gln	Asp	His 660
Gly	Leu	Ile	Val	Ser 665	Gly	Pro	Ser	Lys	Asp 670	Pro	Asp	Leu	Ala	Ser 675
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Gln	Arg	Asp	Trp	Arg 695	Leu	Gln	Thr	Leu	Asn 700	Gly	Ser	His	Ala	Tyr 705
Leu	Thr	Leu	Ala	Leu 710	His	Trp	Val	Glu	Pro 715	Arg	Glu	His	Ile	Ile 720
Pro	Val	Val	Val	Ser 725	His	Asn	Ala	Gln	Met 730	Trp	Gln	Leu	Leu	Val 735
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Lys	Val	Gly	Arg	Met 755	Lys	Gly	Met	Pro	Thr 760	Lys	Leu	Ser	Ala	Val 765
Gly	Ile	Leu	Val	Gly 770	Thr	Leu	Val	Ala	Ile 775	Gly	Ile	Phe	Leu	Ile 780
Leu	Ile	Phe	Thr	His 785	Trp	Thr	Met	Ser	Arg 790	Lys	Lys	Asp	Pro	Asp 795
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<400> 231  
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<212> DNA  
<213> Homo sapiens

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<212> PRT  
<213> Homo sapiens  
  
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Val Arg Asn Gly Asp Glu Ile Ser Lys Leu Ser Gln Leu Val Asn  
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Ser Asn Asn Leu Lys Leu Asn Phe Trp Lys Ser Pro Ser Ser Phe  
50 55 60  
Asn Arg Pro Val Asp Val Leu Val Pro Ser Val Ser Leu Gln Ala  
65 70 75  
Phe Lys Ser Phe Leu Arg Ser Gln Gly Leu Glu Tyr Ala Val Thr  
80 85 90  
Ile Glu Asp Leu Gln Ala Leu Leu Asp Asn Glu Asp Asp Glu Met  
95 100 105  
Gln His Asn Glu Gly Gln Glu Arg Ser Ser Asn Asn Phe Asn Tyr  
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Gly Ala Tyr His Ser Leu Glu Ala Ile Tyr His Glu Met Asp Asn  
125 130 135  
Ile Ala Ala Asp Phe Pro Asp Leu Ala Arg Arg Val Lys Ile Gly  
140 145 150  
His Ser Phe Glu Asn Arg Pro Met Tyr Val Leu Lys Phe Ser Thr  
155 160 165

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His	Ser	Arg	Glu	Trp 185	Ile	Ser	Gln	Ala	Thr 190	Ala	Ile	Trp	Thr	Ala 195
Arg	Lys	Ile	Val	Ser 200	Asp	Tyr	Gln	Arg	Asp 205	Pro	Ala	Ile	Thr	Ser 210
Ile	Leu	Glu	Lys	Met 215	Asp	Ile	Phe	Leu	Leu 220	Pro	Val	Ala	Asn	Pro 225
Asp	Gly	Tyr	Val	Tyr 230	Thr	Gln	Thr	Gln	Asn 235	Arg	Leu	Trp	Arg	Lys 240
Thr	Arg	Ser	Arg	Asn 245	Pro	Gly	Ser	Ser	Cys 250	Ile	Gly	Ala	Asp	Pro 255
Asn	Arg	Asn	Trp	Asn 260	Ala	Ser	Phe	Ala	Gly 265	Lys	Gly	Ala	Ser	Asp 270
Asn	Pro	Cys	Ser	Glu 275	Val	Tyr	His	Gly	Pro 280	His	Ala	Asn	Ser	Glu 285
Val	Glu	Val	Lys	Ser 290	Val	Val	Asp	Phe	Ile 295	Gln	Lys	His	Gly	Asn 300
Phe	Lys	Gly	Phe	Ile 305	Asp	Leu	His	Ser	Tyr 310	Ser	Gln	Leu	Leu	Met 315
Tyr	Pro	Tyr	Gly	Tyr 320	Ser	Val	Lys	Lys	Ala 325	Pro	Asp	Ala	Glu	Glu 330
Leu	Asp	Lys	Val	Ala 335	Arg	Leu	Ala	Ala	Lys 340	Ala	Leu	Ala	Ser	Val 345
Ser	Gly	Thr	Glu	Tyr 350	Gln	Val	Gly	Pro	Thr 355	Cys	Thr	Thr	Val	Tyr 360
Pro	Ala	Ser	Gly	Ser 365	Ser	Ile	Asp	Trp	Ala 370	Tyr	Asp	Asn	Gly	Ile 375
Lys	Phe	Ala	Phe	Thr 380	Phe	Glu	Leu	Arg	Asp 385	Thr	Gly	Thr	Tyr	Gly 390
Phe	Leu	Leu	Pro	Ala 395	Asn	Gln	Ile	Ile	Pro 400	Thr	Ala	Glu	Glu	Thr 405
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<212> DNA
<213> Homo sapiens
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<213> Homo sapiens

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Leu Glu Thr Pro Ser Gln Asn Ile Phe Phe Ser Pro Val Ser Val  
65 70 75

Ser Thr Ser Leu Ala Met Leu Ser Leu Gly Ala His Ser Val Thr  
80 85 90

Lys Thr Gln Ile Leu Gln Gly Leu Gly Phe Asn Leu Thr His Thr  
95 100 105

Pro Glu Ser Ala Ile His Gln Gly Phe Gln His Leu Val His Ser  
110 115 120

Leu Thr Val Pro Ser Lys Asp Leu Thr Leu Lys Met Gly Ser Ala  
125 130 135

Leu Phe Val Lys Lys Glu Leu Gln Leu Gln Ala Asn Phe Leu Gly  
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Asn Val Lys Arg Leu Tyr Glu Ala Glu Val Phe Ser Thr Asp Phe  
155 160 165

Ser Asn Pro Ser Ile Ala Gln Ala Arg Ile Asn Ser His Val Lys  
170 175 180

Lys Lys Thr Gln Gly Lys Val Val Asp Ile Ile Gln Gly Leu Asp  
185 190 195

Leu Leu Thr Ala Met Val Leu Val Asn His Ile Phe Phe Lys Ala



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	215	220	225
Pro Phe Leu Val	Gly Glu Gln Val Thr	Val Gln Val Pro Met	Met
	230	235	240
His Gln Lys Glu	Gln Phe Ala Phe Gly	Val Asp Thr Glu Leu	Asn
	245	250	255
Cys Phe Val Leu	Gln Met Asp Tyr Lys	Gly Asp Ala Val Ala	Phe
	260	265	270
Phe Val Leu Pro	Ser Lys Gly Lys Met	Arg Gln Leu Glu Gln	Ala
	275	280	285
Leu Ser Ala Arg	Thr Leu Ile Lys Trp	Ser His Ser Leu Gln	Lys
	290	295	300
Arg Trp Ile Glu	Val Phe Ile Pro Arg	Phe Ser Ile Ser Ala	Ser
	305	310	315
Tyr Asn Leu Glu	Thr Ile Leu Pro Lys	Met Gly Ile Gln Asn	Ala
	320	325	330
Phe Asp Lys Asn	Ala Asp Phe Ser Gly	Ile Ala Lys Arg Asp	Ser
	335	340	345
Leu Gln Val Ser	Lys Ala Thr His Lys	Ala Val Leu Asp Val	Ser
	350	355	360
Glu Glu Gly Thr	Glu Ala Thr Ala Ala	Thr Thr Thr Lys Phe	Ile
	365	370	375
Val Arg Ser Lys	Asp Gly Pro Ser Tyr	Phe Thr Val Ser Phe	Asn
	380	385	390
Arg Thr Phe Leu	Met Met Ile Thr Asn	Lys Ala Thr Asp Gly	Ile
	395	400	405
Leu Phe Leu Gly	Lys Val Glu Asn Pro	Thr Lys Ser	
	410	415	

<210> 237

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 237

caaccatgca aggacagggc agg 23

<210> 238

<211> 47  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-47  
<223> Synthetic construct.

<400> 238  
ctttgctgtt ggcctctgtg ctcccaacca tgcaaggaca gggcagg 47

<210> 239  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 239  
tgactcgggg tctccaaaac cagc 24

<210> 240  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 240  
ggtataggcg gaaggcaaag tcgg 24

<210> 241  
<211> 48  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-48  
<223> Synthetic construct.

<400> 241  
ggcatcttac ctttatggag tactctttgc tgttggcctc tgtgctcc 48

<210> 242  
<211> 2436  
<212> DNA  
<213> Homo sapiens

<400> 242  
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ctttctcaag	aatcctctgt	tctttgccct	ctaaagtctt	ggtacatcta	200
ggacccaggc	atcttgcttt	ccagccacaa	agagacagat	gaagatgcag	250
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aacaaattcc	aatgagacta	gcacctctgc	caacactgga	tccagtgtga	350
tctccagtgg	agccagcaca	gccaccaact	ctgggtccag	tgtgacctcc	400
agtggggcca	gcacagccac	catctcaggg	tccagcgtga	cctccaatgg	450
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gccaccaact	ctgagtccag	cacaacctcc	agtggggcta	gcacagccac	1500

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 tccagcacia cctccagtgg ggccaacaca gccaccaact ctgggtccag 1650  
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 tcaaaatctc cacagtaaaa tccaaagacc tcaaaaaaaaa aaaaaaaaaa 2400  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 2436

<210> 243  
 <211> 596  
 <212> PRT  
 <213> Homo sapiens

<400> 243  
 Met Lys Met Gln Lys Gly Asn Val Leu Leu Met Phe Gly Leu Leu  
 1 5 10 15  
 Leu His Leu Glu Ala Ala Thr Asn Ser Asn Glu Thr Ser Thr Ser  
 20 25 30  
 Ala Asn Thr Gly Ser Ser Val Ile Ser Ser Gly Ala Ser Thr Ala  
 35 40 45  
 Thr Asn Ser Gly Ser Ser Val Thr Ser Ser Gly Val Ser Thr Ala  
 50 55 60  
 Thr Ile Ser Gly Ser Ser Val Thr Ser Asn Gly Val Ser Ile Val  
 65 70 75

Thr	Asn	Ser	Glu	Phe	His	Thr	Thr	Ser	Ser	Gly	Ile	Ser	Thr	Ala	
				80					85					90	
Thr	Asn	Ser	Glu	Phe	Ser	Thr	Ala	Ser	Ser	Gly	Ile	Ser	Ile	Ala	
				95					100					105	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				110					115					120	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Pro	Ser	Ser	Gly	Ala	Ser	Thr	Val	
				125					130					135	
Thr	Asn	Ser	Gly	Ser	Ser	Val	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				140					145					150	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Arg	Ala	Ser	Thr	Ala	
				155					160					165	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Leu	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				170					175					180	
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				185					190					195	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				200					205					210	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Arg	Ala	Ser	Thr	Ala	
				215					220					225	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				230					235					240	
Thr	Asn	Ser	Glu	Ser	Arg	Thr	Thr	Ser	Asn	Gly	Ala	Gly	Thr	Ala	
				245					250					255	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				260					265					270	
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Val	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				275					280					285	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				290					295					300	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				305					310					315	
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Gly	Thr	Ala	
				320					325					330	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Gly	Ile	Ser	Thr	Val	
				335					340					345	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Pro	Ser	Ser	Gly	Ala	Asn	Thr	Ala	
				350					355					360	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Asn	Thr	Ala	

	365	370	375
Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ala Ser Thr Ala	380	385	390
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Val Ser Thr Ala	395	400	405
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala	410	415	420
Thr Asn Ser Asp Ser Ser Thr Thr Ser Ser Glu Ala Ser Thr Ala	425	430	435
Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ile Ser Thr Val	440	445	450
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Asn Thr Ala	455	460	465
Thr Asn Ser Gly Ser Ser Val Thr Ser Ala Gly Ser Gly Thr Ala	470	475	480
Ala Leu Thr Gly Met His Thr Thr Ser His Ser Ala Ser Thr Ala	485	490	495
Val Ser Glu Ala Lys Pro Gly Gly Ser Leu Val Pro Trp Glu Ile	500	505	510
Phe Leu Ile Thr Leu Val Ser Val Val Ala Ala Val Gly Leu Phe	515	520	525
Ala Gly Leu Phe Phe Cys Val Arg Asn Ser Leu Ser Leu Arg Asn	530	535	540
Thr Phe Asn Thr Ala Val Tyr His Pro His Gly Leu Asn His Gly	545	550	555
Leu Gly Pro Gly Pro Gly Gly Asn His Gly Ala Pro His Arg Pro	560	565	570
Arg Trp Ser Pro Asn Trp Phe Trp Arg Arg Pro Val Ser Ser Ile	575	580	585
Ala Met Glu Met Ser Gly Arg Asn Ser Gly Pro	590	595	

<210> 244

<211> 26

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-26

<223> Synthetic construct.

<400> 244



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 ccagcaagga ggccaaccag ctgctgaatg gcaaccatca aagcggatct 700  
 tccagccatc aaggaggggc cacaaccacg ccgttagcct ctggggcctc 750  
 agtcaacacg cctttcatca accttcccgc cctgtggagg agcgtcgcca 800  
 acatcatgcc ctaaactggc atccggcctt gctgggagaa taatgtcgcc 850  
 gttgtcacat cagctgacat gacctggagg ggttgggggt gggggacagg 900  
 tttctgaaat ccctgaaggg ggttgtactg ggatttgtga ataaacttga 950  
 tacacca 957

<210> 248

<211> 247

<212> PRT

<213> Homo sapiens

<400> 248

Met	His	Leu	Ala	Arg	Leu	Val	Gly	Ser	Cys	Ser	Leu	Leu	Leu	Leu	
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Leu	Gly	Ala	Leu	Ser	Gly	Trp	Ala	Ala	Ser	Asp	Asp	Pro	Ile	Glu	
				20					25					30	
Lys	Val	Ile	Glu	Gly	Ile	Asn	Arg	Gly	Leu	Ser	Asn	Ala	Glu	Arg	
				35					40					45	
Glu	Val	Gly	Lys	Ala	Leu	Asp	Gly	Ile	Asn	Ser	Gly	Ile	Thr	His	
				50					55					60	
Ala	Gly	Arg	Glu	Val	Glu	Lys	Val	Phe	Asn	Gly	Leu	Ser	Asn	Met	
				65					70					75	
Gly	Ser	His	Thr	Gly	Lys	Glu	Leu	Asp	Lys	Gly	Val	Gln	Gly	Leu	
				80					85					90	
Asn	His	Gly	Met	Asp	Lys	Val	Ala	His	Glu	Ile	Asn	His	Gly	Ile	
				95					100					105	
Gly	Gln	Ala	Gly	Lys	Glu	Ala	Glu	Lys	Leu	Gly	His	Gly	Val	Asn	
				110					115					120	
Asn	Ala	Ala	Gly	Gln	Ala	Gly	Lys	Glu	Ala	Asp	Lys	Ala	Val	Gln	
				125					130					135	
Gly	Phe	His	Thr	Gly	Val	His	Gln	Ala	Gly	Lys	Glu	Ala	Glu	Lys	
				140					145					150	
Leu	Gly	Gln	Gly	Val	Asn	His	Ala	Ala	Asp	Gln	Ala	Gly	Lys	Glu	
				155					160					165	
Val	Glu	Lys	Leu	Gly	Gln	Gly	Ala	His	His	Ala	Ala	Gly	Gln	Ala	
				170					175					180	



Gly Lys Glu Leu Gln Asn Ala His Asn Gly Val Asn Gln Ala Ser  
185 190 195

Lys Glu Ala Asn Gln Leu Leu Asn Gly Asn His Gln Ser Gly Ser  
200 205 210

Ser Ser His Gln Gly Gly Ala Thr Thr Thr Pro Leu Ala Ser Gly  
215 220 225

Ala Ser Val Asn Thr Pro Phe Ile Asn Leu Pro Ala Leu Trp Arg  
230 235 240

Ser Val Ala Asn Ile Met Pro  
245

<210> 249

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 249

caatatgcat cttgcacgtc tgg 23

<210> 250

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 250

aagcttctct gcttcctttc ctgc 24

<210> 251

<211> 43

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-43

<223> Synthetic construct.

<400> 251

tgacccatt gagaaggatca ttgaaggat caaccgagg ctg 43

<210> 252

<211> 3781

<212> DNA

<213> Homo sapiens

<400> 252

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tgaccctgac tcactccagg tccggaggcg gggggcccg gggcgactcg 150  
ggggcgacc gcgggcgga gctgccccc gtgagtccgg ccgagccacc 200  
tgagcccgag ccgcgggaca ccgtcgctcc tgctctccga atgctgcgca 250  
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cctcgccac cgctgctgct gctcctgctg ctgctgctcc tgctgcagcc 350  
gccgcctccg acctggggcg tcagccccc gatcagcctg cctctgggct 400  
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<210> 253

<211> 837

<212> PRT

<213> Homo sapiens

<400> 253

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Trp	Gly	Ala	Leu	Pro	Pro	Arg	Pro	Pro	Leu	Leu	Leu	Leu	Leu	Leu
				20					25					30
Leu	Leu	Leu	Leu	Leu	Gln	Pro	Pro	Pro	Pro	Thr	Trp	Ala	Leu	Ser
				35					40					45
Pro	Arg	Ile	Ser	Leu	Pro	Leu	Gly	Ser	Glu	Glu	Arg	Pro	Phe	Leu
				50					55					60
Arg	Phe	Glu	Ala	Glu	His	Ile	Ser	Asn	Tyr	Thr	Ala	Leu	Leu	Leu
				65					70					75
Ser	Arg	Asp	Gly	Arg	Thr	Leu	Tyr	Val	Gly	Ala	Arg	Glu	Ala	Leu

				80				85				90			
Phe	Ala	Leu	Ser	Ser 95	Asn	Leu	Ser	Phe	Leu 100	Pro	Gly	Gly	Glu	Tyr 105	
Gln	Glu	Leu	Leu	Trp 110	Gly	Ala	Asp	Ala	Glu 115	Lys	Lys	Gln	Gln	Cys 120	
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<212> PRT

<213> Homo sapiens

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Lys Gln Met Pro Gln	Tyr Arg Gly Arg Thr	Glu Phe Val Lys Asp			
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Ser Ile Ala Gly Gly	Arg Val Ser Leu Arg	Leu Lys Asn Ile Thr			
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Pro Ser Asp Ile Gly	Leu Tyr Gly Cys Trp	Phe Ser Ser Gln Ile			
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Tyr Asp Glu Glu Ala	Thr Trp Glu Leu Arg	Val Ala Ala Leu Gly			
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Ala Asn Ala Asp Gly	Tyr Ser Leu Tyr Asp	Val Glu Ile Ser Ile			
	185		190		195
Ile Val Gln Glu Asn	Ala Gly Ser Ile Leu	Cys Ser Ile His Leu			
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Ala Glu Gln Ser His	Glu Val Glu Ser Lys	Val Leu Ile Gly Glu			
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Gly Leu Leu Cys Gly	Ala Leu Cys Gly Val	Val Met Gly Met Ile			
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Trp Arg Arg Lys His	Gly Gln Ala Glu Leu	Arg Asp Ala Arg Lys			
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His Ala Val Glu Val	Thr Leu Asp Pro Glu	Thr Ala His Pro Lys			
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Leu Cys Val Ser Asp	Leu Lys Thr Val Thr	His Arg Lys Ala Pro			
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Phe	Asn	Thr	Asn	Asp	Gln	Ser	Leu	Ile	Tyr	Thr	Leu	Leu	Thr	Cys
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Thr	Asp	Lys	Leu	Tyr 65	Ala	Glu	Phe	Gly	Arg 70	Glu	Ala	Ser	Asn	Asn 75
Phe	Thr	Glu	Met	Ser 80	Gln	Arg	Leu	Glu	Ser 85	Met	Val	Lys	Asn	Ala 90
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Lys	Ile	Val	Gln	Leu 140	Val	Leu	His	Glu	Lys 145	Leu	Gln	Asp	Ala	Val 150
Gly	Pro	Pro	Lys	Val 155	Asp	Pro	His	Ser	Val 160	Lys	Ile	Lys	Lys	Ile 165
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Met	Lys	Arg	Gly	Leu	Arg	Arg	Ile	Ile	Val	His	Glu	Lys	Tyr	Lys
				260					265					270
His	Pro	Ser	His	Asp	Tyr	Asp	Ile	Ser	Leu	Ala	Glu	Leu	Ser	Ser
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Pro	Val	Pro	Tyr	Thr	Asn	Ala	Val	His	Arg	Val	Cys	Leu	Pro	Asp
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Phe	Gly	Ala	Leu	Lys	Asn	Asp	Gly	Tyr	Ser	Gln	Asn	His	Leu	Arg
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Gln	Ala	Gln	Val	Thr	Leu	Ile	Asp	Ala	Thr	Thr	Cys	Asn	Glu	Pro
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Gln	Ala	Tyr	Asn	Asp	Ala	Ile	Thr	Pro	Arg	Met	Leu	Cys	Ala	Gly
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Ser	Leu	Glu	Gly	Lys	Thr	Asp	Ala	Cys	Gln	Gly	Asp	Ser	Gly	Gly
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Pro	Leu	Val	Ser	Ser	Asp	Ala	Arg	Asp	Ile	Trp	Tyr	Leu	Ala	Gly
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Ile	Val	Ser	Trp	Gly	Asp	Glu	Cys	Ala	Lys	Pro	Asn	Lys	Pro	Gly
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35 40 45  
Val Pro Cys Asp Tyr Asp His Cys Arg His Leu Gln Val Pro Cys  
50 55 60  
Lys Glu Leu Gln Arg Val Gly Pro Ala Ala Cys Leu Cys Pro Gly  
65 70 75



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<212> PRT

<213> Homo sapiens

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Ile	Ile	Ile	Val	Val	Val	Leu	Ile	Lys	Val	Ile	Leu	Asp	Lys	Tyr	
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Tyr	Phe	Leu	Cys	Gly	Gln	Pro	Leu	His	Phe	Ile	Pro	Arg	Lys	Gln	
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Leu	Ser	Lys	Asp	Arg	Ser	Thr	Leu	Gln	Val	Leu	Asp	Ser	Ala	Thr	
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Ile	Gly	Pro	Asp	Gln	Asp	Leu	Asp	Val	Val	Glu	Ile	Thr	Glu	Asn	
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Ser	Gln	Glu	Leu	Arg	Met	Arg	Asn	Ser	Ser	Gly	Pro	Cys	Leu	Ser	
				170					175					180	
Gly	Ser	Leu	Val	Ser	Leu	His	Cys	Leu	Ala	Cys	Gly	Lys	Ser	Leu	
				185					190					195	
Lys	Thr	Pro	Arg	Val	Val	Gly	Gly	Glu	Glu	Ala	Ser	Val	Asp	Ser	
				200					205					210	
Trp	Pro	Trp	Gln	Val	Ser	Ile	Gln	Tyr	Asp	Lys	Gln	His	Val	Cys	
				215					220					225	
Gly	Gly	Ser	Ile	Leu	Asp	Pro	His	Trp	Val	Leu	Thr	Ala	Ala	His	
				230					235					240	
Cys	Phe	Arg	Lys	His	Thr	Asp	Val	Phe	Asn	Trp	Lys	Val	Arg	Ala	
				245					250					255	

Gly	Ser	Asp	Lys	Leu	Gly	Ser	Phe	Pro	Ser	Leu	Ala	Val	Ala	Lys
				260					265					270
Ile	Ile	Ile	Ile	Glu	Phe	Asn	Pro	Met	Tyr	Pro	Lys	Asp	Asn	Asp
				275					280					285
Ile	Ala	Leu	Met	Lys	Leu	Gln	Phe	Pro	Leu	Thr	Phe	Ser	Gly	Thr
				290					295					300
Val	Arg	Pro	Ile	Cys	Leu	Pro	Phe	Phe	Asp	Glu	Glu	Leu	Thr	Pro
				305					310					315
Ala	Thr	Pro	Leu	Trp	Ile	Ile	Gly	Trp	Gly	Phe	Thr	Lys	Gln	Asn
				320					325					330
Gly	Gly	Lys	Met	Ser	Asp	Ile	Leu	Leu	Gln	Ala	Ser	Val	Gln	Val
				335					340					345
Ile	Asp	Ser	Thr	Arg	Cys	Asn	Ala	Asp	Asp	Ala	Tyr	Gln	Gly	Glu
				350					355					360
Val	Thr	Glu	Lys	Met	Met	Cys	Ala	Gly	Ile	Pro	Glu	Gly	Gly	Val
				365					370					375
Asp	Thr	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Met	Tyr	Gln	Ser
				380					385					390
Asp	Gln	Trp	His	Val	Val	Gly	Ile	Val	Ser	Trp	Gly	Tyr	Gly	Cys
				395					400					405
Gly	Gly	Pro	Ser	Thr	Pro	Gly	Val	Tyr	Thr	Lys	Val	Ser	Ala	Tyr
				410					415					420
Leu	Asn	Trp	Ile	Tyr	Asn	Val	Trp	Lys	Ala	Glu	Leu			
				425					430					

<210> 276  
 <211> 3143  
 <212> DNA  
 <213> Homo sapiens

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 gccattctgg ccttgatat ccaggatcca ggggtccca ggctaaagaa 400





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atggagttgg gggctctctac cagtgcctgg caactgagaa tggcttttca 2000  
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ccagggtcag tgggtggggcc gccctggctg cccagcagtc ctactggccc 2150  
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catcatcctc gtggcctccc cattgagagc actccgggct cggggcaagg 2250  
ttcagggtcg tgagaccctg cgcctgggg agaaggcccc gttaagcaga 2300  
gagcaacacc tccagtctcc caaggaatgc aggacctctg ccagtgatgt 2350  
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<210> 277  
<211> 761  
<212> PRT  
<213> Homo sapiens  
<400> 277

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Ala	Gly	Gly	Gly	Gly	Gln	Gly	Pro	Met	Pro	Arg	Val	Arg	Tyr	Tyr	35	40	45	
Ala	Gly	Asp	Glu	Arg	Arg	Ala	Leu	Ser	Phe	Phe	His	Gln	Lys	Gly	50	55	60	
Leu	Gln	Asp	Phe	Asp	Thr	Leu	Leu	Leu	Ser	Gly	Asp	Gly	Asn	Thr	65	70	75	
Leu	Tyr	Val	Gly	Ala	Arg	Glu	Ala	Ile	Leu	Ala	Leu	Asp	Ile	Gln	80	85	90	
Asp	Pro	Gly	Val	Pro	Arg	Leu	Lys	Asn	Met	Ile	Pro	Trp	Pro	Ala	95	100	105	
Ser	Asp	Arg	Lys	Lys	Ser	Glu	Cys	Ala	Phe	Lys	Lys	Lys	Ser	Asn	110	115	120	
Glu	Thr	Gln	Cys	Phe	Asn	Phe	Ile	Arg	Val	Leu	Val	Ser	Tyr	Asn	125	130	135	
Val	Thr	His	Leu	Tyr	Thr	Cys	Gly	Thr	Phe	Ala	Phe	Ser	Pro	Ala	140	145	150	
Cys	Thr	Phe	Ile	Glu	Leu	Gln	Asp	Ser	Tyr	Leu	Leu	Pro	Ile	Ser	155	160	165	
Glu	Asp	Lys	Val	Met	Glu	Gly	Lys	Gly	Gln	Ser	Pro	Phe	Asp	Pro	170	175	180	
Ala	His	Lys	His	Thr	Ala	Val	Leu	Val	Asp	Gly	Met	Leu	Tyr	Ser	185	190	195	
Gly	Thr	Met	Asn	Asn	Phe	Leu	Gly	Ser	Glu	Pro	Ile	Leu	Met	Arg	200	205	210	
Thr	Leu	Gly	Ser	Gln	Pro	Val	Leu	Lys	Thr	Asp	Asn	Phe	Leu	Arg	215	220	225	
Trp	Leu	His	His	Asp	Ala	Ser	Phe	Val	Ala	Ala	Ile	Pro	Ser	Thr	230	235	240	
Gln	Val	Val	Tyr	Phe	Phe	Phe	Glu	Glu	Thr	Ala	Ser	Glu	Phe	Asp	245	250	255	
Phe	Phe	Glu	Arg	Leu	His	Thr	Ser	Arg	Val	Ala	Arg	Val	Cys	Lys	260	265	270	
Asn	Asp	Val	Gly	Gly	Glu	Lys	Leu	Leu	Gln	Lys	Lys	Trp	Thr	Thr	275	280	285	
Phe	Leu	Lys	Ala	Gln	Leu	Leu	Cys	Thr	Gln	Pro	Gly	Gln	Leu	Pro				

				290					295					300
Phe	Asn	Val	Ile	Arg 305	His	Ala	Val	Leu	Leu 310	Pro	Ala	Asp	Ser	Pro 315
Thr	Ala	Pro	His	Ile 320	Tyr	Ala	Val	Phe	Thr 325	Ser	Gln	Trp	Gln	Val 330
Gly	Gly	Thr	Arg	Ser 335	Ser	Ala	Val	Cys	Ala 340	Phe	Ser	Leu	Leu	Asp 345
Ile	Glu	Arg	Val	Phe 350	Lys	Gly	Lys	Tyr	Lys 355	Glu	Leu	Asn	Lys	Glu 360
Thr	Ser	Arg	Trp	Thr 365	Thr	Tyr	Arg	Gly	Pro 370	Glu	Thr	Asn	Pro	Arg 375
Pro	Gly	Ser	Cys	Ser 380	Val	Gly	Pro	Ser	Ser 385	Asp	Lys	Ala	Leu	Thr 390
Phe	Met	Lys	Asp	His 395	Phe	Leu	Met	Asp	Glu 400	Gln	Val	Val	Gly	Thr 405
Pro	Leu	Leu	Val	Lys 410	Ser	Gly	Val	Glu	Tyr 415	Thr	Arg	Leu	Ala	Val 420
Glu	Thr	Ala	Gln	Gly 425	Leu	Asp	Gly	His	Ser 430	His	Leu	Val	Met	Tyr 435
Leu	Gly	Thr	Thr	Thr 440	Gly	Ser	Leu	His	Lys 445	Ala	Val	Val	Ser	Gly 450
Asp	Ser	Ser	Ala	His 455	Leu	Val	Glu	Glu	Ile 460	Gln	Leu	Phe	Pro	Asp 465
Pro	Glu	Pro	Val	Arg 470	Asn	Leu	Gln	Leu	Ala 475	Pro	Thr	Gln	Gly	Ala 480
Val	Phe	Val	Gly	Phe 485	Ser	Gly	Gly	Val	Trp 490	Arg	Val	Pro	Arg	Ala 495
Asn	Cys	Ser	Val	Tyr 500	Glu	Ser	Cys	Val	Asp 505	Cys	Val	Leu	Ala	Arg 510
Asp	Pro	His	Cys	Ala 515	Trp	Asp	Pro	Glu	Ser 520	Arg	Thr	Cys	Cys	Leu 525
Leu	Ser	Ala	Pro	Asn 530	Leu	Asn	Ser	Trp	Lys 535	Gln	Asp	Met	Glu	Arg 540
Gly	Asn	Pro	Glu	Trp 545	Ala	Cys	Ala	Ser	Gly 550	Pro	Met	Ser	Arg	Ser 555
Leu	Arg	Pro	Gln	Ser 560	Arg	Pro	Gln	Ile	Ile 565	Lys	Glu	Val	Leu	Ala 570
Val	Pro	Asn	Ser	Ile 575	Leu	Glu	Leu	Pro	Cys 580	Pro	His	Leu	Ser	Ala 585

270



<400> 279  
gtctgtgcct ggctgtccac ccag 24

<210> 280  
<211> 45  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-45  
<223> Synthetic construct.

<400> 280  
catcttgtca tgtacctggg aaccaccaca gggctcgctcc acaag 45

<210> 281  
<211> 2320  
<212> DNA  
<213> Homo sapiens

<400> 281  
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ttccttctcc ctggggctct gctctcagag gctgccaaaa tcttgacaat 150  
atctacagta ggtggaagcc attatctact gatggaccgg gtttctcaga 200  
ttcttcaaga tcacgggtcat aatgtcacca tgcttaacca caaaagaggt 250  
ccttttatgc cagattttta aaaggaagaa aaatcatatc aagttatcag 300  
ttggcttgca cctgaagatc atcaaagaga atttaaaaag agttttgatt 350  
tctttctgga agaaacttta ggtggcagag gaaaatttga aaacttatta 400  
aatgttctag aatacttggc gttgcagtgc agtcattttt taaatagaaa 450  
ggatatcatg gattccttaa agaattgagaa ctctgacatg gtgatagttg 500  
aaacttttga ctactgtcct ttcttgattg ctgagaagct tgggaagcca 550  
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aggaggcaac agcacatgca gtctacattt gacaacacca tcaaggaaca 750  
tttcacagaa ggctctaggc cagttttgtc tcatcttcta ctgaaagcag 800  
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<210> 282  
 <211> 523  
 <212> PRT  
 <213> Homo sapiens

<400> 282

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Gly	Val	Leu	Leu	Ser	Glu	Ala	Ala	Lys	Ile	Leu	Thr	Ile	Ser	Thr	20	25	30	
Val	Gly	Gly	Ser	His	Tyr	Leu	Leu	Met	Asp	Arg	Val	Ser	Gln	Ile	35	40	45	
Leu	Gln	Asp	His	Gly	His	Asn	Val	Thr	Met	Leu	Asn	His	Lys	Arg	50	55	60	
Gly	Pro	Phe	Met	Pro	Asp	Phe	Lys	Lys	Glu	Glu	Lys	Ser	Tyr	Gln	65	70	75	
Val	Ile	Ser	Trp	Leu	Ala	Pro	Glu	Asp	His	Gln	Arg	Glu	Phe	Lys	80	85	90	
Lys	Ser	Phe	Asp	Phe	Phe	Leu	Glu	Glu	Thr	Leu	Gly	Gly	Arg	Gly	95	100	105	
Lys	Phe	Glu	Asn	Leu	Leu	Asn	Val	Leu	Glu	Tyr	Leu	Ala	Leu	Gln	110	115	120	
Cys	Ser	His	Phe	Leu	Asn	Arg	Lys	Asp	Ile	Met	Asp	Ser	Leu	Lys	125	130	135	
Asn	Glu	Asn	Phe	Asp	Met	Val	Ile	Val	Glu	Thr	Phe	Asp	Tyr	Cys	140	145	150	
Pro	Phe	Leu	Ile	Ala	Glu	Lys	Leu	Gly	Lys	Pro	Phe	Val	Ala	Ile	155	160	165	
Leu	Ser	Thr	Ser	Phe	Gly	Ser	Leu	Glu	Phe	Gly	Leu	Pro	Ile	Pro	170	175	180	
Leu	Ser	Tyr	Val	Pro	Val	Phe	Arg	Ser	Leu	Leu	Thr	Asp	His	Met	185	190	195	
Asp	Phe	Trp	Gly	Arg	Val	Lys	Asn	Phe	Leu	Met	Phe	Phe	Ser	Phe	200	205	210	
Cys	Arg	Arg	Gln	Gln	His	Met	Gln	Ser	Thr	Phe	Asp	Asn	Thr	Ile	215	220	225	
Lys	Glu	His	Phe	Thr	Glu	Gly	Ser	Arg	Pro	Val	Leu	Ser	His	Leu	230	235	240	
Leu	Leu	Lys	Ala	Glu	Leu	Trp	Phe	Ile	Asn	Ser	Asp	Phe	Ala	Phe	245	250	255	
Asp	Phe	Ala	Arg	Pro	Leu	Leu	Pro	Asn	Thr	Val	Tyr	Val	Gly	Gly				



				260					265					270
Leu	Met	Glu	Lys	Pro 275	Ile	Lys	Pro	Val	Pro 280	Gln	Asp	Leu	Glu	Asn 285
Phe	Ile	Ala	Lys	Phe 290	Gly	Asp	Ser	Gly	Phe 295	Val	Leu	Val	Thr	Leu 300
Gly	Ser	Met	Val	Asn 305	Thr	Cys	Gln	Asn	Pro 310	Glu	Ile	Phe	Lys	Glu 315
Met	Asn	Asn	Ala	Phe 320	Ala	His	Leu	Pro	Gln 325	Gly	Val	Ile	Trp	Lys 330
Cys	Gln	Cys	Ser	His 335	Trp	Pro	Lys	Asp	Val 340	His	Leu	Ala	Ala	Asn 345
Val	Lys	Ile	Val	Asp 350	Trp	Leu	Pro	Gln	Ser 355	Asp	Leu	Leu	Ala	His 360
Pro	Ser	Ile	Arg	Leu 365	Phe	Val	Thr	His	Gly 370	Gly	Gln	Asn	Ser	Ile 375
Met	Glu	Ala	Ile	Gln 380	His	Gly	Val	Pro	Met 385	Val	Gly	Ile	Pro	Leu 390
Phe	Gly	Asp	Gln	Pro 395	Glu	Asn	Met	Val	Arg 400	Val	Glu	Ala	Lys	Lys 405
Phe	Gly	Val	Ser	Ile 410	Gln	Leu	Lys	Lys	Leu 415	Lys	Ala	Glu	Thr	Leu 420
Ala	Leu	Lys	Met	Lys 425	Gln	Ile	Met	Glu	Asp 430	Lys	Arg	Tyr	Lys	Ser 435
Ala	Ala	Val	Ala	Ala 440	Ser	Val	Ile	Leu	Arg 445	Ser	His	Pro	Leu	Ser 450
Pro	Thr	Gln	Arg	Leu 455	Val	Gly	Trp	Ile	Asp 460	His	Val	Leu	Gln	Thr 465
Gly	Gly	Ala	Thr	His 470	Leu	Lys	Pro	Tyr	Val 475	Phe	Gln	Gln	Pro	Trp 480
His	Glu	Gln	Tyr	Leu 485	Phe	Asp	Val	Phe	Val 490	Phe	Leu	Leu	Gly	Leu 495
Thr	Leu	Gly	Thr	Leu 500	Trp	Leu	Cys	Gly	Lys 505	Leu	Leu	Gly	Met	Ala 510
Val	Trp	Trp	Leu	Arg 515	Gly	Ala	Arg	Lys	Val 520	Lys	Glu	Thr		

275

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 283  
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<210> 284  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 284  
tcaggctggt ctccaaagag aggg 24

<210> 285  
<211> 45  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-45  
<223> Synthetic construct.

<400> 285  
cccaaagatg tccacctggc tgcaaattgtg aaaattgtgg actgg 45

<210> 286  
<211> 2340  
<212> DNA  
<213> Homo sapiens

<400> 286  
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gtgctgtccc atccagcagg gctaccctga agctctggct gcagccctcc 200  
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ccagggagag gagcggaaac agaagagggg cagaagaccg gggcacttgt 450

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 cagcgtaccc tgcaggcttc ttctgtgag gaaagccagc atcacggatc 1550  
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 aggctcagcc acaggcagaa ggggtgggaag ggcttgaggt ctgtggctgg 1650  
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 gcatgtatag cagagcagcc agcaggtagc aatcctggct gtccttctat 1750  
 gctggatccc agatggactc tggcccttac ctccccacct gagattaggg 1800  
 tgagtgtgtt tgctctggct gagagcagag ctgagagcag gtatacagag 1850  
 ctggaagtgg accatggaaa acatcgataa ccatgcatcc tcttgcttgg 1900

ccacctcctg aaactgctcc acctttgaag tttgaacttt agtccctcca 1950  
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 cattccttca gaccctctcc tgccagtatg ctaaaccctc cctctctctt 2150  
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 caactagaga atgggtgtca gtgagacact atagaattac taaggagaag 2250  
 atgcctctgg agtttggatc ggggtgttaca ggtacaagta ggtatgttgc 2300  
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<210> 287

<211> 205

<212> PRT

<213> Homo sapiens

<400> 287

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Pro	Gly	Leu	Pro	Leu	Val	Leu	Val	Leu	Leu	Ala	Leu	Gly	Ala	Gly
				20					25					30
Trp	Ala	Gln	Glu	Gly	Ser	Glu	Pro	Val	Leu	Leu	Glu	Gly	Glu	Cys
				35					40					45
Leu	Val	Val	Cys	Glu	Pro	Gly	Arg	Ala	Ala	Ala	Gly	Gly	Pro	Gly
				50					55					60
Gly	Ala	Ala	Leu	Gly	Glu	Ala	Pro	Pro	Gly	Arg	Val	Ala	Phe	Ala
				65					70					75
Ala	Val	Arg	Ser	His	His	His	Glu	Pro	Ala	Gly	Glu	Thr	Gly	Asn
				80					85					90
Gly	Thr	Ser	Gly	Ala	Ile	Tyr	Phe	Asp	Gln	Val	Leu	Val	Asn	Glu
				95					100					105
Gly	Gly	Gly	Phe	Asp	Arg	Ala	Ser	Gly	Ser	Phe	Val	Ala	Pro	Val
				110					115					120
Arg	Gly	Val	Tyr	Ser	Phe	Arg	Phe	His	Val	Val	Lys	Val	Tyr	Asn
				125					130					135
Arg	Gln	Thr	Val	Gln	Val	Ser	Leu	Met	Leu	Asn	Thr	Trp	Pro	Val
				140					145					150
Ile	Ser	Ala	Phe	Ala	Asn	Asp	Pro	Asp	Val	Thr	Arg	Glu	Ala	Ala
				155					160					165
Thr	Ser	Ser	Val	Leu	Leu	Pro	Leu	Asp	Pro	Gly	Asp	Arg	Val	Ser



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<210> 292  
 <211> 388  
 <212> PRT  
 <213> Homo sapiens

<400> 292

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Arg	Ser	Lys	Val	Glu	Lys	Gln	Leu	Gln	Val	Ile	Ser	Val	Leu	Gln
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Trp	Val	Leu	Ser	Phe	Leu	Val	Leu	Gly	Val	Ala	Cys	Ser	Ala	Ile
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Leu	Met	Tyr	Ile	Phe	Cys	Thr	Asp	Cys	Trp	Leu	Ile	Ala	Val	Leu
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Tyr	Phe	Thr	Trp	Leu	Val	Phe	Asp	Trp	Asn	Thr	Pro	Lys	Lys	Gly
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Gly	Arg	Arg	Ser	Gln	Trp	Val	Arg	Asn	Trp	Ala	Val	Trp	Arg	Tyr
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Phe	Arg	Asp	Tyr	Phe	Pro	Ile	Gln	Leu	Val	Lys	Thr	His	Asn	Leu
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Leu	Thr	Thr	Arg	Asn	Tyr	Ile	Phe	Gly	Tyr	His	Pro	His	Gly	Ile
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Met	Gly	Leu	Gly	Ala	Phe	Cys	Asn	Phe	Ser	Thr	Glu	Ala	Thr	Glu
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Val	Ser	Lys	Lys	Phe	Pro	Gly	Ile	Arg	Pro	Tyr	Leu	Ala	Thr	Leu
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Ala	Gly	Asn	Phe	Arg	Met	Pro	Val	Leu	Arg	Glu	Tyr	Leu	Met	Ser
				200					205					210
Gly	Gly	Ile	Cys	Pro	Val	Ser	Arg	Asp	Thr	Ile	Asp	Tyr	Leu	Leu
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Ser	Lys	Asn	Gly	Ser	Gly	Asn	Ala	Ile	Ile	Ile	Val	Val	Gly	Gly
				230					235					240
Ala	Ala	Glu	Ser	Leu	Ser	Ser	Met	Pro	Gly	Lys	Asn	Ala	Val	Thr
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<221> Artificial Sequence  
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<223> Synthetic construct.

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<210> 296  
<211> 3060  
<212> DNA  
<213> Homo sapiens

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gcggctgcag gcttgtccag ccggaagccc tgagggcagc tgttcccact 200  
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cctttttaaa	tttttattat	ttattttatt	atttattttg	agacagggtc	2600

**THE** **NEW** **YORK** **PUBLIC** **LIBRARY**

<211> 368

<213> Homo sapiens

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Val Gln Leu Cys Thr Leu Ala Leu Trp Pro Val Ser Lys Gln Leu  
35 40 45

Tyr Arg Arg Leu Asn Cys Arg Leu Ala Tyr Ser Leu Trp Ser Gln  
50 55 60

Leu Val Met Leu Leu Glu Trp Trp Ser Cys Thr Glu Cys Thr Leu  
65 70 75

Phe Thr Asp Gln Ala Thr Val Glu Arg Phe Gly Lys Glu His Ala  
80 85 90

Val Ile Ile Leu Asn His Asn Phe Glu Ile Asp Phe Leu Cys Gly  
95 100 105

Trp Thr Met Cys Glu Arg Phe Gly Val Leu Gly Ser Ser Lys Val  
110 115 120

Leu Ala Lys Lys Glu Leu Leu Tyr Val Pro Leu Ile Gly Trp Thr  
125 130 135

Trp Tyr Phe Leu Glu Ile Val Phe Cys Lys Arg Lys Trp Glu Glu  
140 145 150

Asp Arg Asp Thr Val Val Glu Gly Leu Arg Arg Leu Ser Asp Tyr  
155 160 165

Pro	Glu	Tyr	Met	Trp 170	Phe	Leu	Leu	Tyr	Cys 175	Glu	Gly	Thr	Arg	Phe 180
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Phe	Thr	Thr	Ala	Val 215	Lys	Cys	Leu	Arg	Gly 220	Thr	Val	Ala	Ala	Val 225
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Ala	Gln	Trp	Leu	His 275	Lys	Leu	Tyr	Gln	Glu 280	Lys	Asp	Ala	Leu	Gln 285
Glu	Ile	Tyr	Asn	Gln 290	Lys	Gly	Met	Phe	Pro 295	Gly	Glu	Gln	Phe	Lys 300
Pro	Ala	Arg	Arg	Pro 305	Trp	Thr	Leu	Leu	Asn 310	Phe	Leu	Ser	Trp	Ala 315
Thr	Ile	Leu	Leu	Ser 320	Pro	Leu	Phe	Ser	Phe 325	Val	Leu	Gly	Val	Phe 330
Ala	Ser	Gly	Ser	Pro 335	Leu	Leu	Ile	Leu	Thr 340	Phe	Leu	Gly	Phe	Val 345
Gly	Ala	Ala	Ser	Phe 350	Gly	Val	Arg	Arg	Leu 355	Ile	Gly	Glu	Ser	Leu 360
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<211> 24
<212> DNA
<213> Artificial
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<223> Synthetic construct.

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<213> Artificial

<223> Synthetic construct.

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<213> Homo sapiens

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<210> 303  
 <211> 1768  
 <212> DNA  
 <213> Homo sapiens

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<210> 306

<211> 262

<212> PRT

<213> Homo sapiens

<400> 306

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Arg	Ser	Met	Arg	Glu	His	Pro	Ala	Leu	Arg	Ser	Leu	Arg	Leu	Leu	65	70	75
Thr	Leu	Glu	Gln	Pro	Gln	Gly	Asp	Ser	Met	Met	Thr	Cys	Glu	Gln	80	85	90
Ala	Gln	Leu	Leu	Ala	Asn	Leu	Ala	Arg	Leu	Ile	Gln	Ala	Lys	Lys	95	100	105
Ala	Leu	Asp	Leu	Gly	Thr	Phe	Thr	Gly	Tyr	Ser	Ala	Leu	Ala	Leu	110	115	120
Ala	Leu	Ala	Leu	Pro	Ala	Asp	Gly	Arg	Val	Val	Thr	Cys	Glu	Val	125	130	135
Asp	Ala	Gln	Pro	Pro	Glu	Leu	Gly	Arg	Pro	Leu	Trp	Arg	Gln	Ala	140	145	150
Glu	Ala	Glu	His	Lys	Ile	Asp	Leu	Arg	Leu	Lys	Pro	Ala	Leu	Glu	155	160	165
Thr	Leu	Asp	Glu	Leu	Leu	Ala	Ala	Gly	Glu	Ala	Gly	Thr	Phe	Asp	170	175	180
Val	Ala	Val	Val	Asp	Ala	Asp	Lys	Glu	Asn	Cys	Ser	Ala	Tyr	Tyr	185	190	195
Glu	Arg	Cys	Leu	Gln	Leu	Leu	Arg	Pro	Gly	Gly	Ile	Leu	Ala	Val	200	205	210
Leu	Arg	Val	Leu	Trp	Arg	Gly	Lys	Val	Leu	Gln	Pro	Pro	Lys	Gly	215	220	225
Asp	Val	Ala	Ala	Glu	Cys	Val	Arg	Asn	Leu	Asn	Glu	Arg	Ile	Arg	230	235	240
Arg	Asp	Val	Arg	Val	Tyr	Ile	Ser	Leu	Leu	Pro	Leu	Gly	Asp	Gly	245	250	255
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<211> 671

<212> PRT

<213> Homo sapiens

<400> 308

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Gly	Ala	Val	Lys	Pro	Pro	Pro	Asn	Lys	Tyr	Pro	Ile	Phe	Phe	Phe
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Gly	Thr	His	Glu	Thr	Ala	Phe	Leu	Gly	Pro	Lys	Asp	Leu	Phe	Pro
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Tyr	Asp	Lys	Cys	Lys	Asp	Lys	Tyr	Gly	Lys	Pro	Asn	Lys	Arg	Lys
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Gly	Phe	Asn	Glu	Gly	Leu	Trp	Glu	Ile	Gln	Asn	Asn	Pro	His	Ala
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Ser	Tyr	Ser	Ala	Pro	Pro	Pro	Val	Ser	Ser	Ser	Asp	Ser	Glu	Ala
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Pro	Glu	Ala	Asn	Pro	Ala	Asp	Gly	Ser	Asp	Ala	Asp	Glu	Asp	Asp
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Glu	Asp	Arg	Gly	Val	Met	Ala	Val	Thr	Ala	Val	Thr	Ala	Thr	Ala
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Ala	Ser	Asp	Arg	Met	Glu	Ser	Asp	Ser	Asp	Ser	Asp	Lys	Ser	Ser
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Asp	Asn	Ser	Gly	Leu	Lys	Arg	Lys	Thr	Pro	Ala	Leu	Lys	Met	Ser
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Val	Ser	Lys	Arg	Ala	Arg	Lys	Ala	Ser	Ser	Asp	Leu	Asp	Gln	Ala
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Ser	Val	Ser	Pro	Ser	Glu	Glu	Glu	Asn	Ser	Glu	Ser	Ser	Ser	Glu
				185					190					195
Ser	Glu	Lys	Thr	Ser	Asp	Gln	Asp	Phe	Thr	Pro	Glu	Lys	Lys	Ala
				200					205					210
Ala	Val	Arg	Ala	Pro	Arg	Arg	Gly	Pro	Leu	Gly	Gly	Arg	Lys	Lys
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Lys	Lys	Ala	Pro	Ser	Ala	Ser	Asp	Ser	Asp	Ser	Lys	Ala	Asp	Ser
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Asp	Gly	Ala	Lys	Pro	Glu	Pro	Val	Ala	Met	Ala	Arg	Ser	Ala	Ser
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Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Asp	Ser	Asp	Val	Ser	Val
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Lys	Lys	Pro	Pro	Arg	Gly	Arg	Lys	Pro	Ala	Glu	Lys	Pro	Leu	Pro
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Lys	Pro	Arg	Gly	Arg	Lys	Pro	Lys	Pro	Glu	Arg	Pro	Pro	Ser	Ser
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Ser	Ser	Ser	Asp	Ser	Asp	Ser	Asp	Glu	Val	Asp	Arg	Ile	Ser	Glu
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Trp	Lys	Arg	Arg	Asp	Glu	Ala	Arg	Arg	Arg	Glu	Leu	Glu	Ala	Arg
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Arg	Arg	Arg	Glu	Gln	Glu	Glu	Glu	Leu	Arg	Arg	Leu	Arg	Glu	Gln
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Arg	Gly	Pro	Pro	Ser	Ser	Ser	Asp	Ser	Glu	Pro	Glu	Ala	Glu	Leu
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				410					415					420
Thr	Glu	Pro	Ala	Arg	Lys	Pro	Gly	Gln	Lys	Glu	Lys	Arg	Val	Arg
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Cys	Leu	Asn	Ala	Leu	Glu	Glu	Leu	Gly	Thr	Leu	Gln	Val	Thr	Ser		500		505		510
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Glu	Ala	Val	Gln	Lys	Val	Asn	Lys	Ala	Gly	Met	Glu	Lys	Glu	Lys		560		565		570
Ala	Glu	Glu	Lys	Leu	Ala	Gly	Glu	Glu	Leu	Ala	Gly	Glu	Glu	Ala		575		580		585
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Cys	Gly	Ser	Ser	Glu	Asp	Leu	His	Asp	Ser	Val	Arg	Glu	Gly	Pro		635		640		645
Asp	Leu	Asp	Arg	Pro	Gly	Ser	Asp	Arg	Gln	Glu	Arg	Glu	Arg	Ala		650		655		660
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<211> 3871

<212> DNA

<213> Homo sapiens

<400> 309

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 Lys Leu Thr Tyr Lys Asp Leu Leu Leu Ser Asn Ser Cys Ile Pro  
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 65 70 75  
 Asp Glu Glu Arg Gly Arg Leu Leu Leu Gly Ala Lys Asp His Ile

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Gly	Lys	Asp	Ala	Asn 125	Thr	Glu	Cys	Ala	Asn 130	Phe	Ile	Arg	Val	Leu 135
Gln	Pro	Tyr	Asn	Lys 140	Thr	His	Ile	Tyr	Val 145	Cys	Gly	Thr	Gly	Ala 150
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Asp	Ile	Ile	Phe	Lys 170	Leu	Asp	Thr	His	Asn 175	Leu	Glu	Ser	Gly	Arg 180
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Thr	Asp	Glu	Tyr	Leu 200	Tyr	Ser	Gly	Thr	Ala 205	Ser	Asp	Phe	Leu	Gly 210
Lys	Asp	Thr	Ala	Phe 215	Thr	Arg	Ser	Leu	Gly 220	Pro	Thr	His	Asp	His 225
His	Tyr	Ile	Arg	Thr 230	Asp	Ile	Ser	Glu	His 235	Tyr	Trp	Leu	Asn	Gly 240
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Cys	Lys	Asn	Asp	Val 290	Gly	Gly	Gln	Arg	Ser 295	Leu	Ile	Asn	Lys	Trp 300
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Thr	Thr	Thr	Ser	Ser 350	Ile	Phe	Lys	Gly	Ser 355	Ala	Val	Cys	Val	Tyr 360
Ser	Met	Ala	Asp	Ile 365	Arg	Ala	Val	Phe	Asn 370	Gly	Pro	Tyr	Ala	His 375

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Ile	Lys	Arg	His	Ser 425	Val	Met	Tyr	Lys	Ser 430	Val	Tyr	Pro	Val	Ala 435
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Ser	Ile	Ser	Lys	Glu 485	Lys	Trp	Asn	Met	Glu 490	Glu	Val	Val	Leu	Glu 495
Glu	Leu	Gln	Ile	Phe 500	Lys	His	Ser	Ser	Ile 505	Ile	Leu	Asn	Met	Glu 510
Leu	Ser	Leu	Lys	Gln 515	Gln	Gln	Leu	Tyr	Ile 520	Gly	Ser	Arg	Asp	Gly 525
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Cys	Ala	Asp	Cys	Cys 545	Leu	Ala	Arg	Asp	Pro 550	Tyr	Cys	Ala	Trp	Asp 555
Gly	Asn	Ala	Cys	Ser 560	Arg	Tyr	Ala	Pro	Thr 565	Ser	Lys	Arg	Arg	Ala 570
Arg	Arg	Gln	Asp	Val 575	Lys	Tyr	Gly	Asp	Pro 580	Ile	Thr	Gln	Cys	Trp 585
Asp	Ile	Glu	Asp	Ser 590	Ile	Ser	His	Glu	Thr 595	Ala	Asp	Glu	Lys	Val 600
Ile	Phe	Gly	Ile	Glu 605	Phe	Asn	Ser	Thr	Phe 610	Leu	Glu	Cys	Ile	Pro 615
Lys	Ser	Gln	Gln	Ala 620	Thr	Ile	Lys	Trp	Tyr 625	Ile	Gln	Arg	Ser	Gly 630
Asp	Glu	His	Arg	Glu 635	Glu	Leu	Lys	Pro	Asp 640	Glu	Arg	Ile	Ile	Lys 645
Thr	Glu	Tyr	Gly	Leu 650	Leu	Ile	Arg	Ser	Leu 655	Gln	Lys	Lys	Asp	Ser 660
Gly	Met	Tyr	Tyr	Cys	Lys	Ala	Gln	Glu	His	Thr	Phe	Ile	His	Thr

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Ile Val Lys Leu Thr Leu Asn Val Ile	Glu Asn Glu Gln Met Glu				
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Asn Thr Gln Arg Ala Glu His Glu Glu	Gly Gln Val Lys Asp Leu				
695	700			705	
Leu Ala Glu Ser Arg Leu Arg Tyr Lys	Asp Tyr Ile Gln Ile Leu				
710	715			720	
Ser Ser Pro Asn Phe Ser Leu Asp Gln	Tyr Cys Glu Gln Met Trp				
725	730			735	
His Arg Glu Lys Arg Arg Gln Arg Asn	Lys Gly Gly Pro Lys Trp				
740	745			750	
Lys His Met Gln Glu Met Lys Lys Lys	Arg Asn Arg Arg His His				
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Arg Asp Leu Asp Glu Leu Pro Arg Ala	Val Ala Thr				
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 <222> 1-25  
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<211> 370

&lt;212&gt; PRT

<213> Homo sapiens

<400> 315

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Gln	Arg	Leu	Glu	Gln 35	Arg	Arg	Gln	Gln	Ala 40	Ser	Glu	Arg	Glu	Ala 45
Pro	Ser	Ile	Glu	Gln 50	Arg	Leu	Gln	Glu	Val 55	Arg	Glu	Ser	Ile	Arg 60
Arg	Ala	Gln	Val	Ser 65	Gln	Val	Lys	Gly	Ala 70	Ala	Arg	Leu	Ala	Leu 75
Leu	Gln	Gly	Ala	Gly 80	Leu	Asp	Val	Glu	Arg 85	Trp	Leu	Lys	Pro	Ala 90
Met	Thr	Gln	Ala	Gln 95	Asp	Glu	Val	Glu	Gln 100	Glu	Arg	Arg	Leu	Ser 105
Glu	Ala	Arg	Leu	Ser 110	Gln	Arg	Asp	Leu	Ser 115	Pro	Thr	Ala	Glu	Asp 120
Ala	Glu	Leu	Ser	Asp 125	Phe	Glu	Glu	Cys	Glu 130	Glu	Thr	Gly	Glu	Leu 135
Phe	Glu	Glu	Pro	Ala 140	Pro	Gln	Ala	Leu	Ala 145	Thr	Arg	Ala	Leu	Pro 150
Cys	Pro	Ala	His	Val 155	Val	Phe	Arg	Tyr	Gln 160	Ala	Gly	Arg	Glu	Asp 165
Glu	Leu	Thr	Ile	Thr 170	Glu	Gly	Glu	Trp	Leu 175	Glu	Val	Ile	Glu	Glu 180
Gly	Asp	Ala	Asp	Glu 185	Trp	Val	Lys	Ala	Arg 190	Asn	Gln	His	Gly	Glu 195
Val	Gly	Phe	Val	Pro 200	Glu	Arg	Tyr	Leu	Asn 205	Phe	Pro	Asp	Leu	Ser 210
Leu	Pro	Glu	Ser	Ser 215	Gln	Asp	Ser	Asp	Asn 220	Pro	Cys	Gly	Ala	Glu 225
Pro	Thr	Ala	Phe	Leu 230	Ala	Gln	Ala	Leu	Tyr 235	Ser	Tyr	Thr	Gly	Gln 240
Ser	Ala	Glu	Glu	Leu 245	Ser	Phe	Pro	Glu	Gly 250	Ala	Leu	Ile	Arg	Leu 255
Leu	Pro	Arg	Ala	Gln 260	Asp	Gly	Val	Asp	Asp 265	Gly	Phe	Trp	Arg	Gly 270
Glu	Phe	Gly	Gly	Arg 275	Val	Gly	Val	Phe	Pro 280	Ser	Leu	Leu	Val	Glu 285
Glu	Leu	Leu	Gly	Pro 290	Pro	Gly	Pro	Pro	Glu 295	Leu	Ser	Asp	Pro	Glu 300
Gln	Met	Leu	Pro	Ser	Pro	Ser	Pro	Pro	Ser	Phe	Ser	Pro	Pro	Ala



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Asp Lys Ala Leu	Asp Phe Pro Gly Phe	Leu Asp Met Met Ala Pro			
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Arg Leu Arg Pro	Met Arg Pro Pro Pro	Pro Pro Pro Ala Lys Ala			
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Pro Asp Pro Gly	His Pro Asp Pro Leu Thr				
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<213> Homo sapiens

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Leu	Arg	Arg	Lys	Ser 185	Pro	Ala	Ser	Gly	Gln	Gly	Pro	Met	Cys	Asn 195
Val	Lys	Ala	Pro	Leu 200	Gly	Ser	Pro	Ser	Pro	Arg	Pro	Arg	Arg	Ala 210
Lys	Arg	Phe	Ala	Ser 215	Leu	Ser	Arg	Phe	Val	Glu	Thr	Leu	Val	Val 225
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Tyr	Leu	Leu	Thr	Val 245	Met	Ala	Ala	Ala	Ala	Lys	Ala	Phe	Lys	His 255
Pro	Ser	Ile	Arg	Asn 260	Pro	Val	Ser	Leu	Val	Val	Thr	Arg	Leu	Val 270
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Ala	Gln	Thr	Leu	Arg 290	Ser	Phe	Cys	Ala	Trp	Gln	Arg	Gly	Leu	Asn 300
Thr	Pro	Glu	Asp	Ser 305	Gly	Pro	Asp	His	Phe	Asp	Thr	Ala	Ile	Leu 315
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Gly	Met	Ala	Asp	Val 335	Gly	Thr	Val	Cys	Asp	Pro	Ala	Arg	Ser	Cys 345
Ala	Ile	Val	Glu	Asp 350	Asp	Gly	Leu	Gln	Ser	Ala	Phe	Thr	Ala	Ala 360
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Pro	Cys	Ile	Ser	Leu 380	Asn	Gly	Pro	Leu	Ser	Thr	Ser	Arg	His	Val 390
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Gly	His	Cys	Leu	Leu 425	Asp	Lys	Pro	Glu	Ala	Pro	Leu	His	Leu	Pro 435

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				455					460					465	
Pro	Cys	Ala	Ala	Leu	Trp	Cys	Ser	Gly	His	Leu	Asn	Gly	His	Ala	
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Gln	Cys	Ala	Ala	Tyr	Asn	His	Arg	Thr	Asp	Leu	Phe	Lys	Ser	Phe	
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Ser	Phe	Arg	Lys	Phe	Arg	Tyr	Gly	Tyr	Asn	Asn	Val	Val	Thr	Ile	
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Pro	Ala	Gly	Ala	Thr	His	Ile	Leu	Val	Arg	Gln	Gln	Gly	Asn	Pro	
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<211> 1197  
<212> DNA  
<213> Homo sapiens

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ttgtggactg gtgtttggta tcttggccct aactctaatt gtctgtttt 200  
gggggagcaa gcacttctgg ccggaggtag ccaaaaaagc ctatgacatg 250  
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<210> 322



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Population	1,000,000	1,050,000	1,100,000	1,150,000	1,200,000	1,250,000	1,300,000	1,350,000	1,400,000	1,450,000	1,500,000	1,550,000	1,600,000	1,650,000	1,700,000	1,750,000	1,800,000	1,850,000	1,900,000	1,950,000	2,000,000	2,050,000	2,100,000	2,150,000	2,200,000	2,250,000	2,300,000	2,350,000	2,400,000	2,450,000	2,500,000	2,550,000	2,600,000	2,650,000	2,700,000	2,750,000	2,800,000	2,850,000	2,900,000	2,950,000	3,000,000	3,050,000	3,100,000	3,150,000	3,200,000	3,250,000	3,300,000	3,350,000	3,400,000	3,450,000	3,500,000	3,550,000	3,600,000	3,650,000	3,700,000	3,750,000	3,800,000	3,850,000	3,900,000	3,950,000	4,000,000	4,050,000	4,100,000	4,150,000	4,200,000	4,250,000	4,300,000	4,350,000	4,400,000	4,450,000	4,500,000	4,550,000	4,600,000	4,650,000	4,700,000	4,750,000	4,800,000	4,850,000	4,900,000	4,950,000	5,000,000	5,050,000	5,100,000	5,150,000	5,200,000	5,250,000	5,300,000	5,350,000	5,400,000	5,450,000	5,500,000	5,550,000	5,600,000	5,650,000	5,700,000	5,750,000	5,800,000	5,850,000	5,900,000	5,950,000	6,000,000	6,050,000	6,100,000	6,150,000	6,200,000	6,250,000	6,300,000	6,350,000	6,400,000	6,450,000	6,500,000	6,550,000	6,600,000	6,650,000	6,700,000	6,750,000	6,800,000	6,850,000	6,900,000	6,950,000	7,000,000	7,050,000	7,100,000	7,150,000	7,200,000	7,250,000	7,300,000	7,350,000	7,400,000	7,450,000	7,500,000	7,550,000	7,600,000	7,650,000	7,700,000	7,750,000	7,80																																																																

Met Ala Lys Asn Pro Pro Glu Asn Cys Glu Asp Cys His Ile Leu  
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Ile Cys Gly Leu Val Phe Gly Ile Leu Ala Leu Thr Leu Ile Val  
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Leu Phe Trp Gly Ser Lys His Phe Trp Pro Glu Val Pro Lys Lys  
50 55 60

Ala Tyr Asp Met Glu His Thr Phe Tyr Ser Asn Gly Glu Lys Lys  
65 70 75

Lys Ile Tyr Met Glu Ile Asp Pro Val Thr Arg Thr Glu Ile Phe  
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Arg Ser Gly Asn Gly Thr Asp Glu Thr Leu Glu Val His Asp Phe  
95 100 105

Lys Asn Gly Tyr Thr Gly Ile Tyr Phe Val Gly Leu Gln Lys Cys  
110 115 120

Phe Ile Lys Thr Gln Ile Lys Val Ile Pro Glu Phe Ser Glu Pro  
125 130 135

Glu Glu Glu Ile Asp Glu Asn Glu Glu Ile Thr Thr Thr Phe Phe  
140 145 150

Glu Gln Ser Val Ile Trp Val Pro Ala Glu Lys Pro Ile Glu Asn  
155 160 165

Arg Asp Phe Leu Lys Asn Ser Lys Ile Leu Glu Ile Cys Asp Asn  
170 175 180

Val	Thr	Met	Tyr	Trp	Ile	Asn	Pro	Thr	Leu	Ile	Ser	Val	Ser	Glu
				185					190					195

Leu Gln Asp Phe Glu Glu Glu Gly Glu Asp Leu His Phe Pro Ala  
200 205 210

Asn Glu Lys Lys Gly Ile Glu Gln Asn Glu Gln Trp Val Val Pro  
215 220 225

Gln Val Lys Val Glu Lys Thr Arg His Ala Arg Gln Ala Ser Glu  
230 235 240

Glu Glu Leu Pro Ile Asn Asp Tyr Thr Glu Asn Gly Ile Glu Phe  
245 250 255

Asp Pro Met Leu Asp Glu Arg Gly Tyr Cys Cys Ile Tyr Cys Arg  
260 265 270

Arg Gly Asn Arg Tyr Cys Arg Arg Val Cys Glu Pro Leu Leu Gly  
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Tyr Tyr Pro Tyr Pro Tyr Cys Tyr Gln Gly Gly Arg Val Ile Cys  
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Arg Val Ile Met Pro Cys Asn Trp Trp Val Ala Arg Met Leu Gly  
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<210> 323

<211> 1174

<212> DNA

<213> Homo sapiens

<400> 323

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<210> 324

<211> 239

<212> PRT

<213> Homo sapiens

<400> 324

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				20					25					30
Arg	Arg	Thr	Ala	His	Val	Gly	Thr	Asn	Ile	Leu	Thr	Ala	Val	Ser
				35					40					45
Tyr	Leu	Lys	Gly	Leu	Trp	Met	Glu	Cys	Val	Trp	His	Ser	Thr	Gly
				50					55					60
Ile	Tyr	Gln	Cys	Gln	Ile	Tyr	Arg	Ser	Leu	Leu	Ala	Leu	Pro	Gln
				65					70					75
Asp	Leu	Gln	Ala	Ala	Arg	Ala	Leu	Met	Val	Ile	Ser	Cys	Leu	Leu
				80					85					90
Ser	Gly	Ile	Ala	Cys	Ala	Cys	Ala	Val	Ile	Gly	Met	Lys	Cys	Thr
				95					100					105
Arg	Cys	Ala	Lys	Gly	Thr	Pro	Ala	Lys	Thr	Thr	Phe	Ala	Ile	Leu
				110					115					120
Gly	Gly	Thr	Leu	Phe	Ile	Leu	Ala	Gly	Leu	Leu	Cys	Met	Val	Ala
				125					130					135
Val	Ser	Trp	Thr	Thr	Asn	Asp	Val	Val	Gln	Asn	Phe	Tyr	Asn	Pro
				140					145					150
Leu	Leu	Pro	Ser	Gly	Met	Lys	Phe	Glu	Ile	Gly	Gln	Ala	Leu	Tyr
				155					160					165
Leu	Gly	Phe	Ile	Ser	Ser	Ser	Leu	Ser	Leu	Ile	Gly	Gly	Thr	Leu
				170					175					180
Leu	Cys	Leu	Ser	Cys	Gln	Asp	Glu	Ala	Pro	Tyr	Arg	Pro	Tyr	Gln
				185					190					195
Ala	Pro	Pro	Arg	Ala	Thr	Thr	Thr	Thr	Ala	Asn	Thr	Ala	Pro	Ala
				200					205					210
Tyr	Gln	Pro	Pro	Ala	Ala	Tyr	Lys	Asp	Asn	Arg	Ala	Pro	Ser	Val
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 <211> 2121  
 <212> DNA  
 <213> Homo sapiens

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 gagccatgat cacaccactg cactccagcc aggtgacata gcgagatcct 2050  
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<210> 326  
 <211> 261  
 <212> PRT  
 <213> Homo sapiens

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 35 40 45  
 Tyr Glu Gly Leu Trp Arg Ser Cys Val Arg Gln Ser Ser Gly Phe  
 50 55 60  
 Thr Glu Cys Arg Pro Tyr Phe Thr Ile Leu Gly Leu Pro Ala Met  
 65 70 75  
 Leu Gln Ala Val Arg Ala Leu Met Ile Val Gly Ile Val Leu Gly

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80	85	90
Ala Ile Gly Leu Leu Val Ser Ile Phe	Ala Leu Lys Cys Ile Arg	
95	100	105
Ile Gly Ser Met Glu Asp Ser Ala Lys	Ala Asn Met Thr Leu Thr	
110	115	120
Ser Gly Ile Met Phe Ile Val Ser Gly	Leu Cys Ala Ile Ala Gly	
125	130	135
Val Ser Val Phe Ala Asn Met Leu Val	Thr Asn Phe Trp Met Ser	
140	145	150
Thr Ala Asn Met Tyr Thr Gly Met Gly	Gly Met Val Gln Thr Val	
155	160	165
Gln Thr Arg Tyr Thr Phe Gly Ala Ala	Leu Phe Val Gly Trp Val	
170	175	180
Ala Gly Gly Leu Thr Leu Ile Gly Gly	Val Met Met Cys Ile Ala	
185	190	195
Cys Arg Gly Leu Ala Pro Glu Glu Thr	Asn Tyr Lys Ala Val Ser	
200	205	210
Tyr His Ala Ser Gly His Ser Val Ala	Tyr Lys Pro Gly Gly Phe	
215	220	225
Lys Ala Ser Thr Gly Phe Gly Ser Asn	Thr Lys Asn Lys Lys Ile	
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Tyr Asp Gly Gly Ala Arg Thr Glu Asp	Glu Val Gln Ser Tyr Pro	
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Ser Lys His Asp Tyr Val		
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 <211> 2010  
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 atcgcacaa ccaaaaaagt tatcacaccg gaaagaagtc accgagcgtc 750  
 tactccagaa gtcagtatgt gtagttgtgt atgttttttt aactttacta 800  
 taaagccatg caaatgacaa aaatctatat tactttctca aaatggaccc 850  
 caaagaaact ttgatttact gttcttaact gcctaattct aattacagga 900  
 actgtgcac agctatttat gattctataa gctatttcag cagaatgaga 950  
 tattaacccc aatgctttga ttgttctaga aagtatagta atttgttttc 1000  
 taaggtggtt caagcatcta ctctttttat catttacttc aaaatgacat 1050  
 tgctaaagac tgcattattt tactactgta atttctccac gacatagcat 1100  
 tatgtacata gatgagtgtg acatttatat ctccataga gacatgctta 1150  
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 ctattaattg tttaaaaaca gottagggat taatgtctc catttataat 1300  
 gaagattaaa atgaaggctt taatcagcat tgtaaaggaa attgaatggc 1350  
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 <212> PRT  
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<400> 328

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Arg	Val	Ser	Ala	Phe	Ile	Glu	Asn	Asn	Ile	Val	Val	Phe	Glu	Asn	35	40	45	
Phe	Trp	Glu	Gly	Leu	Trp	Met	Asn	Cys	Val	Arg	Gln	Ala	Asn	Ile	50	55	60	
Arg	Met	Gln	Cys	Lys	Ile	Tyr	Asp	Ser	Leu	Leu	Ala	Leu	Ser	Pro	65	70	75	
Asp	Leu	Gln	Ala	Ala	Arg	Gly	Leu	Met	Cys	Ala	Ala	Ser	Val	Met	80	85	90	
Ser	Phe	Leu	Ala	Phe	Met	Met	Ala	Ile	Leu	Gly	Met	Lys	Cys	Thr	95	100	105	
Arg	Cys	Thr	Gly	Asp	Asn	Glu	Lys	Val	Lys	Ala	His	Ile	Leu	Leu	110	115	120	
Thr	Ala	Gly	Ile	Ile	Phe	Ile	Ile	Thr	Gly	Met	Val	Val	Leu	Ile	125	130	135	
Pro	Val	Ser	Trp	Val	Ala	Asn	Ala	Ile	Ile	Arg	Asp	Phe	Tyr	Asn	140	145	150	
Ser	Ile	Val	Asn	Val	Ala	Gln	Lys	Arg	Glu	Leu	Gly	Glu	Ala	Leu	155	160	165	
Tyr	Leu	Gly	Trp	Thr	Thr	Ala	Leu	Val	Leu	Ile	Val	Gly	Gly	Ala	170	175	180	
Leu	Phe	Cys	Cys	Val	Phe	Cys	Cys	Asn	Glu	Lys	Ser	Ser	Ser	Tyr	185	190	195	
Arg	Tyr	Ser	Ile	Pro	Ser	His	Arg	Thr	Thr	Gln	Lys	Ser	Tyr	His	200	205	210	





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tgttttgtta gtgca 1315

<210> 330

<211> 220

<212> PRT

<213> Homo sapiens

<400> 330

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			20						25					30

Lys	Val	Thr	Ala	Phe	Ile	Gly	Asn	Ser	Ile	Val	Val	Ala	Gln	Val
			35						40					45

Val	Trp	Glu	Gly	Leu	Trp	Met	Ser	Cys	Val	Val	Gln	Ser	Thr	Gly
			50						55					60

Gln	Met	Gln	Cys	Lys	Val	Tyr	Asp	Ser	Leu	Leu	Ala	Leu	Pro	Gln
			65						70					75

Asp	Leu	Gln	Ala	Ala	Arg	Ala	Leu	Cys	Val	Ile	Ala	Leu	Leu	Val
			80						85					90

Ala	Leu	Phe	Gly	Leu	Leu	Val	Tyr	Leu	Ala	Gly	Ala	Lys	Cys	Thr
			95						100					105

Thr	Cys	Val	Glu	Glu	Lys	Asp	Ser	Lys	Ala	Arg	Leu	Val	Leu	Thr
			110						115					120

Ser	Gly	Ile	Val	Phe	Val	Ile	Ser	Gly	Val	Leu	Thr	Leu	Ile	Pro
			125						130					135

Val	Cys	Trp	Thr	Ala	His	Ala	Ile	Ile	Arg	Asp	Phe	Tyr	Asn	Pro
			140						145					150

Leu	Val	Ala	Glu	Ala	Gln	Lys	Arg	Glu	Leu	Gly	Ala	Ser	Leu	Tyr
			155						160					165

Leu	Gly	Trp	Ala	Ala	Ser	Gly	Leu	Leu	Leu	Leu	Gly	Gly	Gly	Leu
			170						175					180

Leu	Cys	Cys	Thr	Cys	Pro	Ser	Gly	Gly	Ser	Gln	Gly	Pro	Ser	His
			185						190					195

Tyr	Met	Ala	Arg	Tyr	Ser	Thr	Ser	Ala	Pro	Ala	Ile	Ser	Arg	Gly
			200						205					210

Pro	Ser	Glu	Tyr	Pro	Thr	Lys	Asn	Tyr	Val
			215						220

<210> 331

<211> 1160

<212> DNA

<213> Homo sapiens

<400> 331

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cgggccctca tgtgtgtggc tgttgctctc tccttgatcg ccttgcttat 400  
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cgaaagtctc aatttggtac tgggtgtagg aatgaaaatg acttacttgg 950  
acattctgac ttcaggtgta ttaaattgcat tgactattgt tggaccaat 1000  
cgctgctcca attttcatat tctaaattca agtataacca taatcattag 1050  
caagtgtaca atgatggact acttattact ttttgaccat catgtattat 1100  
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acctattcta 1160

<210> 332

<211> 173

<212> PRT

<213> Homo sapiens

<400> 332

Met Asn Cys Ile Arg Gln Ala Arg Val Arg Leu Gln Cys Lys Phe



Feature "392" on 1

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<211> 85  
<212> PRT  
<213> Homo sapiens

<400> 334  
Met Lys Ile Thr Gly Gly Leu Leu Leu Cys Thr Val Val Tyr  
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Phe Cys Ser Ser Ser Glu Ala Ala Ser Leu Ser Pro Lys Lys Val  
20 25 30  
Asp Cys Ser Ile Tyr Lys Lys Tyr Pro Val Val Ala Ile Pro Cys  
35 40 45  
Pro Ile Thr Tyr Leu Pro Val Cys Gly Ser Asp Tyr Ile Thr Tyr  
50 55 60  
Gly Asn Glu Cys His Leu Cys Thr Glu Ser Leu Lys Ser Asn Gly  
65 70 75  
Arg Val Gln Phe Leu His Asp Gly Ser Cys  
80 85

<210> 335  
<211> 742  
<212> DNA  
<213> Homo sapiens

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tggccctgac cgggctggcg ctgctcctgc tcctgtgctg gggcccaggt 150  
ggcataagtg gaaataaaact caagctgatg cttcaaaaac gagaagcacc 200  
tggtccaact aagactaaag tggccgttga tgagaataaa gccaaagaat 250  
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cccgaggtgc agcagtggta ccagcagttt ctctacatgg gctttgatga 350  
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gacatgaata ctatggcgat tactaccaac gtcactatga tgaagactct 450  
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ctacgatgac tactaaccat gacttgccac acgctgtaca agaagcaaat 550  
agcgattctc ttcattgtatc tcctaattgcc ttacactact tggtttctga 600

tttgctctat ttcagcagat cttttctacc tactttgtgt gatcaaaaaa 650  
gaagagttaa aacaacacat gtaaatgcct tttgatattt catgggaatg 700  
cctctcattt aaaaatagaa ataaagcatt ttgttaaaaa ga 742

<210> 336  
<211> 148  
<212> PRT  
<213> Homo sapiens

<400> 336  
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20 25 30  
Gly Asn Lys Leu Lys Leu Met Leu Gln Lys Arg Glu Ala Pro Val  
35 40 45  
Pro Thr Lys Thr Lys Val Ala Val Asp Glu Asn Lys Ala Lys Glu  
50 55 60  
Phe Leu Gly Ser Leu Lys Arg Gln Lys Arg Gln Leu Trp Asp Arg  
65 70 75  
Thr Arg Pro Glu Val Gln Gln Trp Tyr Gln Gln Phe Leu Tyr Met  
80 85 90  
Gly Phe Asp Glu Ala Lys Phe Glu Asp Asp Ile Thr Tyr Trp Leu  
95 100 105  
Asn Arg Asp Arg Asn Gly His Glu Tyr Tyr Gly Asp Tyr Tyr Gln  
110 115 120  
Arg His Tyr Asp Glu Asp Ser Ala Ile Gly Pro Arg Ser Pro Tyr  
125 130 135  
Gly Phe Arg His Gly Ala Ser Val Asn Tyr Asp Asp Tyr  
140 145

<210> 337  
<211> 1310  
<212> DNA  
<213> Homo sapiens

<400> 337  
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tgaaggggtg ggtgatgagg tgaccgtcct tttctcggtg cttgcctgcc 150  
ttctggtgct ggcccttgcc tgggtotcaa cgcacaccgc tgaggggcggg 200  
gaccactgc ccagccgctc agggacccca acgcatccc agccagcgc 250

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gggttcacag	caacaccgcc	agccccggac	tccccgcagg	agcccctcgt	400
gctacggctg	aaattcctca	atgattcaga	gcaggtggcc	agggcctggc	450
cccacgacac	cattggctcc	ttgaaaagga	cccagtttcc	cggccgggaa	500
cagcagggtgc	gactcatcta	ccaagggcag	ctgctaggcg	acgacaccca	550
gaccctgggc	agccttcacc	tccctcccaa	ctgcgttctc	cactgccacg	600
tgtccacgag	agtcgggtccc	ccaaatcccc	cctgccccgc	ggggtccgag	650
cccggcccct	ccgggctgga	aatcggcagc	ctgctgctgc	ccctgctgct	700
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gccagccct	gcgcgcgaga	ggactcccgc	gactggcgga	ggccccgccc	1000
tgcgaccgcc	ggggctcggg	gccacctccc	ggggctgctg	aacctcagcc	1050
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gccccgggca	gagccggggc	gccccggggg	ccgtcttag	tgttctgccg	1150
gaggaccag	ccgcctccaa	tccctgacag	ctccttgggc	tgagttgggg	1200
acgccaggtc	ggtgggaggc	tggtgaaggg	gagcggggag	gggcagagga	1250
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<210> 338

$\langle 211 \rangle$  246

<212> PRT

<213> Homo sapiens

<400> 338

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Ser Val Leu Ala Cys Leu Leu Val Leu Ala Leu Ala Trp Val Ser  
20 25 30

Thr His Thr Ala Glu Gly Gly Asp Pro Leu Pro Gln Pro Ser Gly  
35 40 45

Thr	Pro	Thr	Pro	Ser	Gln	Pro	Ser	Ala	Ala	Met	Ala	Ala	Thr	Asp	
				50					55					60	
Ser	Met	Arg	Gly	Glu	Ala	Pro	Gly	Ala	Glu	Thr	Pro	Ser	Leu	Arg	
				65					70					75	
His	Arg	Gly	Gln	Ala	Ala	Gln	Pro	Glu	Pro	Ser	Thr	Gly	Phe	Thr	
				80					85					90	
Ala	Thr	Pro	Pro	Ala	Pro	Asp	Ser	Pro	Gln	Glu	Pro	Leu	Val	Leu	
				95					100					105	
Arg	Leu	Lys	Phe	Leu	Asn	Asp	Ser	Glu	Gln	Val	Ala	Arg	Ala	Trp	
				110					115					120	
Pro	His	Asp	Thr	Ile	Gly	Ser	Leu	Lys	Arg	Thr	Gln	Phe	Pro	Gly	
				125					130					135	
Arg	Glu	Gln	Gln	Val	Arg	Leu	Ile	Tyr	Gln	Gly	Gln	Leu	Leu	Gly	
				140					145					150	
Asp	Asp	Thr	Gln	Thr	Leu	Gly	Ser	Leu	His	Leu	Pro	Pro	Asn	Cys	
				155					160					165	
Val	Leu	His	Cys	His	Val	Ser	Thr	Arg	Val	Gly	Pro	Pro	Asn	Pro	
				170					175					180	
Pro	Cys	Pro	Pro	Gly	Ser	Glu	Pro	Gly	Pro	Ser	Gly	Leu	Glu	Ile	
				185					190					195	
Gly	Ser	Leu	Leu	Leu	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	
				200					205					210	
Trp	Tyr	Cys	Gln	Ile	Gln	Tyr	Arg	Pro	Phe	Phe	Pro	Leu	Thr	Ala	
				215					220					225	
Thr	Leu	Gly	Leu	Ala	Gly	Phe	Thr	Leu	Leu	Leu	Ser	Leu	Leu	Ala	
				230					235					240	
Phe	Ala	Met	Tyr	Arg	Pro										
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<210> 339  
 <211> 849  
 <212> DNA  
 <213> Homo sapiens

<400> 339  
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 caagacccta agaaccatca gccctcagct gcacctctc ccctccaagg 150  
 atgacaaagg cgctactcat ctatttggtc agcagctttc ttgccctaaa 200  
 tcaggccagc ctcacagtc gctgtgactt ggcccaggtg ctgcagctgg 250





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<210> 345
<211> 45
<212> DNA
<213> Artificial
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<220>  
<221> Artificial Sequence  
<222> 1-45  
<223> Synthetic construct.

<400> 345  
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<210> 346  
<211> 2575  
<212> DNA  
<213> Homo sapiens

<400> 346  
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actgagaacc caccagctca tcccagacac ctcatagcaa cctattttata 100  
caaaggggga aagaaacacc tgagcagaat ggaatcatta tttttttccc 150  
aaggagaaaa ccggggtaaa gggaggggaag caattcaatt tgaagtccct 200  
gtgaatgggc tttcagaagg caattaaaga aatccactca gagaggactt 250  
ggggtgaaac ttgggtcctg tggttttctg attgtaagtg gaagcaggtc 300  
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aaacttccag gtggaacaag caacctatgt tctgctgcaa gcttgaagga 400  
gcctggagcg ggagaaagct aacttgaaca tgacctgttg catttggcaa 450  
gttctagcaa catgctccta aggaagcgat acaggcacag accatgcaga 500  
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 cttcatggat gccactgcg agtgccaccc aggttggtg gagccctcc 1350  
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<210> 347

<211> 639

<212> PRT

<213> Homo sapiens

<400> 347

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Phe	Leu	Leu	Leu	Leu	Leu	Met	Leu	Gly	Cys	Val	Leu	Met	Met	Val
				20					25					30
Ala	Met	Leu	His	Pro	Pro	His	His	Thr	Leu	His	Gln	Thr	Val	Thr
				35					40					45
Ala	Gln	Ala	Ser	Lys	His	Ser	Pro	Glu	Ala	Arg	Tyr	Arg	Leu	Asp
				50					55					60
Phe	Gly	Glu	Ser	Gln	Asp	Trp	Val	Leu	Glu	Ala	Glu	Asp	Glu	Gly
				65					70					75
Glu	Glu	Tyr	Ser	Pro	Leu	Glu	Gly	Leu	Pro	Pro	Phe	Ile	Ser	Leu
				80					85					90
Arg	Glu	Asp	Gln	Leu	Leu	Val	Ala	Val	Ala	Leu	Pro	Gln	Ala	Arg
				95					100					105
Arg	Asn	Gln	Ser	Gln	Gly	Arg	Arg	Gly	Gly	Ser	Tyr	Arg	Leu	Ile
				110					115					120
Lys	Gln	Pro	Arg	Arg	Gln	Asp	Lys	Glu	Ala	Pro	Lys	Arg	Asp	Trp
				125					130					135
Gly	Ala	Asp	Glu	Asp	Gly	Glu	Val	Ser	Glu	Glu	Glu	Glu	Leu	Thr
				140					145					150
Pro	Phe	Ser	Leu	Asp	Pro	Arg	Gly	Leu	Gln	Glu	Ala	Leu	Ser	Ala
				155					160					165
Arg	Ile	Pro	Leu	Gln	Arg	Ala	Leu	Pro	Glu	Val	Arg	His	Pro	Leu
				170					175					180
Cys	Leu	Gln	Gln	His	Pro	Gln	Asp	Ser	Leu	Pro	Thr	Ala	Ser	Val
				185					190					195
Ile	Leu	Cys	Phe	His	Asp	Glu	Ala	Trp	Ser	Thr	Leu	Leu	Arg	Thr
				200					205					210
Val	His	Ser	Ile	Leu	Asp	Thr	Val	Pro	Arg	Ala	Phe	Leu	Lys	Glu
				215					220					225
Ile	Ile	Leu	Val	Asp	Asp	Leu	Ser	Gln	Gln	Gly	Gln	Leu	Lys	Ser
				230					235					240
Ala	Leu	Ser	Glu	Tyr	Val	Ala	Arg	Leu	Glu	Gly	Val	Lys	Leu	Leu
				245					250					255

Arg	Ser	Asn	Lys	Arg 260	Leu	Gly	Ala	Ile	Arg 265	Ala	Arg	Met	Leu	Gly 270
Ala	Thr	Arg	Ala	Thr 275	Gly	Asp	Val	Leu	Val 280	Phe	Met	Asp	Ala	His 285
Cys	Glu	Cys	His	Pro 290	Gly	Trp	Leu	Glu	Pro 295	Leu	Leu	Ser	Arg	Ile 300
Ala	Gly	Asp	Arg	Ser 305	Arg	Val	Val	Ser	Pro 310	Val	Ile	Asp	Val	Ile 315
Asp	Trp	Lys	Thr	Phe 320	Gln	Tyr	Tyr	Pro	Ser 325	Lys	Asp	Leu	Gln	Arg 330
Gly	Val	Leu	Asp	Trp 335	Lys	Leu	Asp	Phe	His 340	Trp	Glu	Pro	Leu	Pro 345
Glu	His	Val	Arg	Lys 350	Ala	Leu	Gln	Ser	Pro 355	Ile	Ser	Pro	Ile	Arg 360
Ser	Pro	Val	Val	Pro 365	Gly	Glu	Val	Val	Ala 370	Met	Asp	Arg	His	Tyr 375
Phe	Gln	Asn	Thr	Gly 380	Ala	Tyr	Asp	Ser	Leu 385	Met	Ser	Leu	Arg	Gly 390
Gly	Glu	Asn	Leu	Glu 395	Leu	Ser	Phe	Lys	Ala 400	Trp	Leu	Cys	Gly	Gly 405
Ser	Val	Glu	Ile	Leu 410	Pro	Cys	Ser	Arg	Val 415	Gly	His	Ile	Tyr	Gln 420
Asn	Gln	Asp	Ser	His 425	Ser	Pro	Leu	Asp	Gln 430	Glu	Ala	Thr	Leu	Arg 435
Asn	Arg	Val	Arg	Ile 440	Ala	Glu	Thr	Trp	Leu 445	Gly	Ser	Phe	Lys	Glu 450
Thr	Phe	Tyr	Lys	His 455	Ser	Pro	Glu	Ala	Phe 460	Ser	Leu	Ser	Lys	Ala 465
Glu	Lys	Pro	Asp	Cys 470	Met	Glu	Arg	Leu	Gln 475	Leu	Gln	Arg	Arg	Leu 480
Gly	Cys	Arg	Thr	Phe 485	His	Trp	Phe	Leu	Ala 490	Asn	Val	Tyr	Pro	Glu 495
Leu	Tyr	Pro	Ser	Glu 500	Pro	Arg	Pro	Ser	Phe 505	Ser	Gly	Lys	Leu	His 510
Asn	Thr	Gly	Leu	Gly 515	Leu	Cys	Ala	Asp	Cys 520	Gln	Ala	Glu	Gly	Asp 525
Ile	Leu	Gly	Cys	Pro 530	Met	Val	Leu	Ala	Pro 535	Cys	Ser	Asp	Ser	Arg 540
Gln	Gln	Gln	Tyr	Leu	Gln	His	Thr	Ser	Arg	Lys	Glu	Ile	His	Phe



<210> 351  
<211> 2524  
<212> DNA  
<213> Homo sapiens

<400> 351  
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tccctctctg gccactgctg ttgctgcccc tcccaccgcc tgctcagggc 150  
tcttcattcct cccctcgaac cccaccagcc ccagcccgcc ccccgctgtgc 200  
caggggaggg ccctcggccc cacgtcatgt gtgcgtgtgg gagcgagcac 250  
ctccaccaag ccgatctcct cgggtcccaa gatcacgtcg gcaagtcctg 300  
cctggcactg cacccccagc caccocatca ggctttgagg aggggccgcc 350  
ctcatcccaa tacccttggg ctatcgtgtg gggcccacc gtgtctcgag 400  
aggatggagg ggacccaac tctgccaatc cgggatttct ggactatggt 450  
tttgagccc ctcatgggct cgcaacccca caccccaact cagactccat 500  
gcgaggtgat ggagatgggc ttatccttgg agaggcacct gccaccctgc 550  
ggccattcct gttcgggggc cgtggggaag gtgtggaccc ccagctctat 600  
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cttcaagttc tgctgggacc gcagccagaa gcgacgcaga ccctcagggc 700  
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caactctgcc ctotaaacct tgattcccc tctttgtctt gaacttcccc 1200  
ttctattctg gcctaccctt tggttcctga ctgtgccctt tccctcttcc 1250  
tctcaggatt cccctgggtga atctgtgatg cccccaatgt tgggggtgcag 1300



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<210> 352

<211> 243

<212> PRT

<213> Homo sapiens

<400> 352

Met Arg Pro Gln Gly Pro Ala Ala Ser Pro Gln Arg Leu Arg Gly  
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Ser	Glu	Ile	Pro	Lys 35	Gly	Lys	Gln	Lys	Ala 40	Gln	Leu	Arg	Gln	Arg 45
Glu	Val	Val	Asp	Leu 50	Tyr	Asn	Gly	Met	Cys 55	Leu	Gln	Gly	Pro	Ala 60
Gly	Val	Pro	Gly	Arg 65	Asp	Gly	Ser	Pro	Gly 70	Ala	Asn	Val	Ile	Pro 75
Gly	Thr	Pro	Gly	Ile 80	Pro	Gly	Arg	Asp	Gly 85	Phe	Lys	Gly	Glu	Lys 90
Gly	Glu	Cys	Leu	Arg 95	Glu	Ser	Phe	Glu	Glu 100	Ser	Trp	Thr	Pro	Asn 105
Tyr	Lys	Gln	Cys	Ser 110	Trp	Ser	Ser	Leu	Asn 115	Tyr	Gly	Ile	Asp	Leu 120
Gly	Lys	Ile	Ala	Glu 125	Cys	Thr	Phe	Thr	Lys 130	Met	Arg	Ser	Asn	Ser 135
Ala	Leu	Arg	Val	Leu 140	Phe	Ser	Gly	Ser	Leu 145	Arg	Leu	Lys	Cys	Arg 150
Asn	Ala	Cys	Cys	Gln 155	Arg	Trp	Tyr	Phe	Thr 160	Phe	Asn	Gly	Ala	Glu 165
Cys	Ser	Gly	Pro	Leu 170	Pro	Ile	Glu	Ala	Ile 175	Ile	Tyr	Leu	Asp	Gln 180
Gly	Ser	Pro	Glu	Met 185	Asn	Ser	Thr	Ile	Asn 190	Ile	His	Arg	Thr	Ser 195
Ser	Val	Glu	Gly	Leu 200	Cys	Glu	Gly	Ile	Gly 205	Ala	Gly	Leu	Val	Asp 210
Val	Ala	Ile	Trp	Val 215	Gly	Thr	Cys	Ser	Asp 220	Tyr	Pro	Lys	Gly	Asp 225
Ala	Ser	Thr	Gly	Trp 230	Asn	Ser	Val	Ser	Arg 235	Ile	Ile	Ile	Glu	Glu 240

Leu Pro Lys

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<400> 353
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cggccaggat ggcatactgt ctggccctgc gcattggcgt gctgctggtc 100
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tccgggggttc tggcccctgc ggtgctcaca gacgatgttc cacaggagcc 150  
 cgtgcccacg ctgtggaacg agccggccga gctgccgtcg ggagaaggcc 200  
 ccgtggagag caccagcccc ggccgggagc ccgtggacac cggcccccca 250  
 gccccaccg tcgcgccagg acccgaggac agcaccgcgc aggagcggct 300  
 ggaccagggc ggcgggtcgc tggggcccgg cgctatcgcg gccatcgtga 350  
 tcgccgccct gctggccacc tgcgtggtgc tggcgctcgt ggtcgtcgcg 400  
 ctgagaaagt tttctgcctc ctgaagcgaa taaaggggcc gcgcccggcc 450  
 gcggcgcgac tcggcaaaaa aaaaaaaaaa 480

<210> 354

<211> 121

<212> PRT

<213> Homo sapiens

<400> 354

Met	Ala	Ser	Cys	Leu	Ala	Leu	Arg	Met	Ala	Leu	Leu	Leu	Val	Ser
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Gly	Val	Leu	Ala	Pro	Ala	Val	Leu	Thr	Asp	Asp	Val	Pro	Gln	Glu
				20					25					30
Pro	Val	Pro	Thr	Leu	Trp	Asn	Glu	Pro	Ala	Glu	Leu	Pro	Ser	Gly
				35					40					45
Glu	Gly	Pro	Val	Glu	Ser	Thr	Ser	Pro	Gly	Arg	Glu	Pro	Val	Asp
				50					55					60
Thr	Gly	Pro	Pro	Ala	Pro	Thr	Val	Ala	Pro	Gly	Pro	Glu	Asp	Ser
				65					70					75
Thr	Ala	Gln	Glu	Arg	Leu	Asp	Gln	Gly	Gly	Gly	Ser	Leu	Gly	Pro
				80					85					90
Gly	Ala	Ile	Ala	Ala	Ile	Val	Ile	Ala	Ala	Leu	Leu	Ala	Thr	Cys
				95					100					105
Val	Val	Leu	Ala	Leu	Val	Val	Val	Ala	Leu	Arg	Lys	Phe	Ser	Ala
				110					115					120

Ser

<210> 355

<211> 2134

<212> DNA

<213> Homo sapiens

<400> 355

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gtgcctgacg	gcggcgctgg	cccacggctg	tctgcaactgc	cacagcaact	150
tctccaagaa	gttctccttc	taccgccacc	atgtgaactt	caagtctctgg	200
tgggtggggc	acatccccgt	gtcagggggc	ctgctcaccg	actggagcga	250
cgacacgatg	aaggagctgc	acctggccat	ccccgccaa	atcacccggg	300
agaagctgga	ccaagtggcg	acagcagtgt	accagatgat	ggatcagctg	350
taccagggga	agatgtactt	ccccgggtat	ttccccaacg	agctgcgaaa	400
catcttccgg	gagcaggtgc	acctcatcca	gaacgccatc	atcgaaaggc	450
acctggcacc	aggcagctgg	ggaggagggc	agctctccag	ggaggggacc	500
agcctagcac	ctgaaggatc	aatgccatca	ccccgcgggg	acctccccta	550
agtagcccc	agaggcgctg	ggagtgttgc	caccgccctc	ccctgaagtt	600
tgtctcatct	cacgtggggg	gtcaacctgg	ggaccccttc	cctccggggc	650
atggacacac	atacatgaaa	accaggccgc	atcgactgtc	agcaccgctg	700
tggcatcttc	cagtacgaga	ccatctcctg	caacaactgc	acagactcgc	750
acgtcgcttg	ctttggctat	aactgcgagt	agggtctcagg	catcacaccc	800
accctgcca	gggccctact	gtccctgggg	tcccaggctc	tccttgaggg	850
gggtccccg	ccttccacct	ggctgtcatc	gggtagggcg	gggccgtggg	900
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tggaagtcag	ctgtccaggg	cctcctgaac	tacataaata	actggcacia	1000
gtaagtcccc	tcctcaaacc	aacacaggca	gtgtgtgtat	gtgagcacct	1050
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cctgggacac acagagccac cccggccttg tgagtgaccc agagaaggga 1600  
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 gcacaccctt cggacatccc aggcacgagg gtgtcgtgga tgtggccaca 1700  
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 aacctgacct tggaagatgc tgctgagtgt ctcaagcagc actgacagca 1900  
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 cctgcctgtc actctggagc tgggctgctg ctgcctcagg accccctctc 2000  
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 ctgcgggatg tgattaaagt ccctgatgtt tctc 2134

<210> 356  
 <211> 157  
 <212> PRT  
 <213> Homo sapiens

<400> 356  
 Met Ala Leu Leu Leu Cys Leu Val Cys Leu Thr Ala Ala Leu Ala  
 1 5 10 15  
 His Gly Cys Leu His Cys His Ser Asn Phe Ser Lys Lys Phe Ser  
 20 25 30  
 Phe Tyr Arg His His Val Asn Phe Lys Ser Trp Trp Val Gly Asp  
 35 40 45  
 Ile Pro Val Ser Gly Ala Leu Leu Thr Asp Trp Ser Asp Asp Thr  
 50 55 60  
 Met Lys Glu Leu His Leu Ala Ile Pro Ala Lys Ile Thr Arg Glu  
 65 70 75  
 Lys Leu Asp Gln Val Ala Thr Ala Val Tyr Gln Met Met Asp Gln  
 80 85 90  
 Leu Tyr Gln Gly Lys Met Tyr Phe Pro Gly Tyr Phe Pro Asn Glu  
 95 100 105  
 Leu Arg Asn Ile Phe Arg Glu Gln Val His Leu Ile Gln Asn Ala  
 110 115 120  
 Ile Ile Glu Arg His Leu Ala Pro Gly Ser Trp Gly Gly Gly Gln  
 125 130 135  
 Leu Ser Arg Glu Gly Pro Ser Leu Ala Pro Glu Gly Ser Met Pro

140

145

150

Ser Pro Arg Gly Asp Leu Pro  
155

&lt;210&gt; 357

&lt;211&gt; 1536

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 357

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acagatgtcc cagctgccat ggaattcatt gctgccactg aggtggctgt 200  
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gttgaaactc taccttcttt cataagcaca tgtcogtctc tgactcagga 1350  
tcaaaaacca aaggatggtt ttaaacacct ttgtgaaatt gtctttttgc 1400  
cagaagttaa aggctgtctc caagtccctg aactcagcag aaatagacca 1450  
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caacctgcat aataaataaa aggcaatcat gttata 1536

<210> 358

<211> 273

<212> PRT

<213> Homo sapiens

<400> 358

Met	Glu	Ala	Ala	Pro	Ser	Arg	Phe	Met	Phe	Leu	Leu	Phe	Leu	Leu	1	5	10	15
Thr	Cys	Glu	Leu	Ala	Ala	Glu	Val	Ala	Ala	Glu	Val	Glu	Lys	Ser	20	25	30	
Ser	Asp	Gly	Pro	Gly	Ala	Ala	Gln	Glu	Pro	Thr	Trp	Leu	Thr	Asp	35	40	45	
Val	Pro	Ala	Ala	Met	Glu	Phe	Ile	Ala	Ala	Thr	Glu	Val	Ala	Val	50	55	60	
Ile	Gly	Phe	Phe	Gln	Asp	Leu	Glu	Ile	Pro	Ala	Val	Pro	Ile	Leu	65	70	75	
His	Ser	Met	Val	Gln	Lys	Phe	Pro	Gly	Val	Ser	Phe	Gly	Ile	Ser	80	85	90	
Thr	Asp	Ser	Glu	Val	Leu	Thr	His	Tyr	Asn	Ile	Thr	Gly	Asn	Thr	95	100	105	
Ile	Cys	Leu	Phe	Arg	Leu	Val	Asp	Asn	Glu	Gln	Leu	Asn	Leu	Glu	110	115	120	
Asp	Glu	Asp	Ile	Glu	Ser	Ile	Asp	Ala	Thr	Lys	Leu	Ser	Arg	Phe	125	130	135	
Ile	Glu	Ile	Asn	Ser	Leu	His	Met	Val	Thr	Glu	Tyr	Asn	Pro	Val	140	145	150	
Thr	Val	Ile	Gly	Leu	Phe	Asn	Ser	Val	Ile	Gln	Ile	His	Leu	Leu	155	160	165	
Leu	Ile	Met	Asn	Lys	Ala	Ser	Pro	Glu	Tyr	Glu	Glu	Asn	Met	His	170	175	180	
Arg	Tyr	Gln	Lys	Ala	Ala	Lys	Leu	Phe	Gln	Gly	Lys	Ile	Leu	Phe	185	190	195	

Ile	Leu	Val	Asp	Ser	Gly	Met	Lys	Glu	Asn	Gly	Lys	Val	Ile	Ser
				200					205					210
Phe	Phe	Lys	Leu	Lys	Glu	Ser	Gln	Leu	Pro	Ala	Leu	Ala	Ile	Tyr
				215					220					225
Gln	Thr	Leu	Asp	Asp	Glu	Trp	Asp	Thr	Leu	Pro	Thr	Ala	Glu	Val
				230					235					240
Ser	Val	Glu	His	Val	Gln	Asn	Phe	Cys	Asp	Gly	Phe	Leu	Ser	Gly
				245					250					255
Lys	Leu	Leu	Lys	Glu	Asn	Arg	Glu	Ser	Glu	Gly	Lys	Thr	Pro	Lys
				260					265					270

Val Glu Leu

<210> 359  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 359  
 ccagcagtgc ccatactcca tagc 24

<210> 360  
 <211> 20  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-20  
 <223> Synthetic construct.

<400> 360  
 tgacgagtgg gatacactgc 20

<210> 361  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 361  
 gctctacgga aacttctgct gtgg 24

<210> 362



<211> 50  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-50  
<223> Synthetic construct.

<400> 362  
attcccaggc gtgtcatttg ggatcagcac tgattctgag gttctgacac 50

<210> 363  
<211> 1777  
<212> DNA  
<213> Homo sapiens

<400> 363  
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cctcagcggg gacccgggct cagggacgcg gcggcggcgg cggcgactgc 150  
agtggctgga cgatggcagc gtccgccgga gccggggcgg tgattgcagc 200  
cccagacagc cggcgctggc tgtggtcggg gctggcggcg gcgcttgggc 250  
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gggcgcgacac tactgtgtcg tttttccact actccaagg gcaagtgtac 450  
cttggggaatt atccaccatt taaagacaga atcagctggg ctggagacct 500  
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gcaggctcct cggaagtccc cctccgacac tgagggtctt gtaaagagtc 850  
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tcggcgggac atcacagtga caagattaac aagtcagagt ctgtggtgta 950  
tgcggatatc cgaaagaatt aagagaatac ctagaacata tcctcagcaa 1000



Arg	Ile	Ser	Trp	Ala	Gly	Asp	Leu	Asp	Lys	Lys	Asp	Ala	Ser	Ile	110	115	120
Asn	Ile	Glu	Asn	Met	Gln	Phe	Ile	His	Asn	Gly	Thr	Tyr	Ile	Cys	125	130	135
Asp	Val	Lys	Asn	Pro	Pro	Asp	Ile	Val	Val	Gln	Pro	Gly	His	Ile	140	145	150
Arg	Leu	Tyr	Val	Val	Glu	Lys	Glu	Asn	Leu	Pro	Val	Phe	Pro	Val	155	160	165
Trp	Val	Val	Val	Gly	Ile	Val	Thr	Ala	Val	Val	Leu	Gly	Leu	Thr	170	175	180
Leu	Leu	Ile	Ser	Met	Ile	Leu	Ala	Val	Leu	Tyr	Arg	Arg	Lys	Asn	185	190	195
Ser	Lys	Arg	Asp	Tyr	Thr	Gly	Cys	Ser	Thr	Ser	Glu	Ser	Leu	Ser	200	205	210
Pro	Val	Lys	Gln	Ala	Pro	Arg	Lys	Ser	Pro	Ser	Asp	Thr	Glu	Gly	215	220	225
Leu	Val	Lys	Ser	Leu	Pro	Ser	Gly	Ser	His	Gln	Gly	Pro	Val	Ile	230	235	240
Tyr	Ala	Gln	Leu	Asp	His	Ser	Gly	Gly	His	His	Ser	Asp	Lys	Ile	245	250	255
Asn	Lys	Ser	Glu	Ser	Val	Val	Tyr	Ala	Asp	Ile	Arg	Lys	Asn		260	265	

<210> 365

<211> 1321

<212> DNA

<213> Homo sapiens

<400> 365

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aggggcgcgg ccccggcgca gtccccgcg gcccccgacc ctgaggcgctc 250

gcctctggcc gagccgccac aggagcagtc cctcgccccg tggctctccgc 300

agaccccggc gccgccctgc tccaggtgct tcgccagagc catcgagagc 350

agccgcgacc tgctgcacag gatcaaggat gaggtgggcg caccgggcat 400

agtggttgga gtttctgtag atggaaaaga agtctggtca gaaggttttag 450

gttatgctga tgttgagaac cgtgtaccat gtaaaccaga gacagttatg 500

cgaattgcta gcatcagcaa aagtctcacc atggttgctc ttgccaaatt 550  
 gtgggaagca gggaaactgg atcttgatat tccagtacaa cattatgttc 600  
 ccgaattccc agaaaaagaa tatgaagggtg aaaagggttc tgtcacaaca 650  
 agattactga tttcccatTT aagtggaatt cgtcattatg aaaaggacat 700  
 aaaaaagggtg aaagaagaga aagcttataa agccttgaag atgatgaaag 750  
 agaatgtttgc atttgagcaa gaaaaagaag gcaaaagtaa tgaaaagaat 800  
 gattttacta aattttaaac agagcaggag aatgaagcca aatgccggaa 850  
 ttcaaaacct ggcaagaaaa agaatgattt tgaacaaggc gaattatatt 900  
 tgagagaaaa gtttgaaaat tcaattgaat ccctaagatt atttaaaaat 950  
 gatcctttgt tcttcaaacc tggtagtcag tttttgtatt caacttttgg 1000  
 ctatacccta ctggcagcca tagtagagag agcttcagga tgtaaattatt 1050  
 tggactatat gcagaaaata ttccatgact tggatatgct gacgactgtg 1100  
 caggaagaaa acgagccagt gatttacaat agagcaagggt aaatgaatac 1150  
 cttctgctgt gtctagctat atcgcatctt aacactatTT tattaattaa 1200  
 aagtcaaatt ttctttgttt ccattccaaa atcaacctgc cacatttttg 1250  
 gagcttttct acatgtctgt tttctcatct gtaaagtga ggaagtaaaa 1300  
 catgtttata aagtaaaaaa a 1321

<210> 366  
 <211> 373  
 <212> PRT  
 <213> Homo sapiens

<400> 366  
 Met Tyr Arg Leu Leu Ser Ala Val Thr Ala Arg Ala Ala Ala Pro  
 1 5 10 15  
 Gly Gly Leu Ala Ser Ser Cys Gly Arg Arg Gly Val His Gln Arg  
 20 25 30  
 Ala Gly Leu Pro Pro Leu Gly His Gly Trp Val Gly Gly Leu Gly  
 35 40 45  
 Leu Gly Leu Gly Leu Ala Leu Gly Val Lys Leu Ala Gly Gly Leu  
 50 55 60  
 Arg Gly Ala Ala Pro Ala Gln Ser Pro Ala Ala Pro Asp Pro Glu  
 65 70 75  
 Ala Ser Pro Leu Ala Glu Pro Pro Gln Glu Gln Ser Leu Ala Pro  
 80 85 90

Trp	Ser	Pro	Gln	Thr	Pro	Ala	Pro	Pro	Cys	Ser	Arg	Cys	Phe	Ala	
				95					100					105	
Arg	Ala	Ile	Glu	Ser	Ser	Arg	Asp	Leu	Leu	His	Arg	Ile	Lys	Asp	
				110					115					120	
Glu	Val	Gly	Ala	Pro	Gly	Ile	Val	Val	Gly	Val	Ser	Val	Asp	Gly	
				125					130					135	
Lys	Glu	Val	Trp	Ser	Glu	Gly	Leu	Gly	Tyr	Ala	Asp	Val	Glu	Asn	
				140					145					150	
Arg	Val	Pro	Cys	Lys	Pro	Glu	Thr	Val	Met	Arg	Ile	Ala	Ser	Ile	
				155					160					165	
Ser	Lys	Ser	Leu	Thr	Met	Val	Ala	Leu	Ala	Lys	Leu	Trp	Glu	Ala	
				170					175					180	
Gly	Lys	Leu	Asp	Leu	Asp	Ile	Pro	Val	Gln	His	Tyr	Val	Pro	Glu	
				185					190					195	
Phe	Pro	Glu	Lys	Glu	Tyr	Glu	Gly	Glu	Lys	Val	Ser	Val	Thr	Thr	
				200					205					210	
Arg	Leu	Leu	Ile	Ser	His	Leu	Ser	Gly	Ile	Arg	His	Tyr	Glu	Lys	
				215					220					225	
Asp	Ile	Lys	Lys	Val	Lys	Glu	Glu	Lys	Ala	Tyr	Lys	Ala	Leu	Lys	
				230					235					240	
Met	Met	Lys	Glu	Asn	Val	Ala	Phe	Glu	Gln	Glu	Lys	Glu	Gly	Lys	
				245					250					255	
Ser	Asn	Glu	Lys	Asn	Asp	Phe	Thr	Lys	Phe	Lys	Thr	Glu	Gln	Glu	
				260					265					270	
Asn	Glu	Ala	Lys	Cys	Arg	Asn	Ser	Lys	Pro	Gly	Lys	Lys	Lys	Asn	
				275					280					285	
Asp	Phe	Glu	Gln	Gly	Glu	Leu	Tyr	Leu	Arg	Glu	Lys	Phe	Glu	Asn	
				290					295					300	
Ser	Ile	Glu	Ser	Leu	Arg	Leu	Phe	Lys	Asn	Asp	Pro	Leu	Phe	Phe	
				305					310					315	
Lys	Pro	Gly	Ser	Gln	Phe	Leu	Tyr	Ser	Thr	Phe	Gly	Tyr	Thr	Leu	
				320					325					330	
Leu	Ala	Ala	Ile	Val	Glu	Arg	Ala	Ser	Gly	Cys	Lys	Tyr	Leu	Asp	
				335					340					345	
Tyr	Met	Gln	Lys	Ile	Phe	His	Asp	Leu	Asp	Met	Leu	Thr	Thr	Val	
				350					355					360	
Gln	Glu	Glu	Asn	Glu	Pro	Val	Ile	Tyr	Asn	Arg	Ala	Arg			
				365					370						

<210> 367

<211> 30  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-30  
 <223> Synthetic construct.

<400> 367  
 tggaaaagaa gtctggtcag aaggtttagg 30

<210> 368  
 <211> 25  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-25  
 <223> Synthetic construct.

<400> 368  
 catttggtt cattctcctg ctctg 25

<210> 369  
 <211> 28  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-28  
 <223> Synthetic construct.

<400> 369  
 aaaacctcag aacaactcat ttgcacc 28

<210> 370  
 <211> 41  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-41  
 <223> Synthetic construct.

<400> 370  
 gtctcaccat ggttgctctt gccaaattgt gggaagcagg g 41

<210> 371  
 <211> 1150  
 <212> DNA  
 <213> Homo sapiens

<400> 371  
 gtgacactat agaagagcta tgacgtcgca tgcacgcgta cgtaagctcg 50

gaattcggct	cgaggctggg	gggaagaagc	cgagatggcg	gcagccagcg	100
ctggggcaac	ccggctgctc	ctgctcttgc	tgatggcggt	agcagcgccc	150
agtcgagccc	ggggcagcgg	ctgccggggc	gggactgggt	cgcgagggggc	200
tggggcgga	ggtcgagagg	gcgaggcctg	tggcacgggt	gggctgctgc	250
tggagcactc	atttgagatc	gatgacagtg	ccaacttccg	gaagcggggc	300
tcactgctct	ggaaccagca	ggatggtacc	ttgtccctgt	cacagcggca	350
gctcagcgag	gaggagcggg	gccgactccg	ggatgtggca	gccctgaatg	400
gcctgtaccg	ggtcgggatc	ccaaggcgac	ccggggccct	ggatggcctg	450
gaagctggtg	gctatgtctc	ctcctttgtc	cctgctgtgt	ccctgggtgga	500
gtcgcacctg	tgggaccagc	tgaccctgca	cgtgggatgtg	gccggcaacg	550
tgggtgggct	gtcgggtggg	acgcaccccg	ggggctgccg	gggccatgag	600
gtggaggacg	tggacctgga	gctgttcaac	acctcggtgc	agctgcagcc	650
gcccaccaca	gcccagggc	ctgagacggc	ggccttcatt	gagcgcttgg	700
agatggaaca	ggcccagaag	gccaagaacc	cccaggagca	gaagtccttc	750
ttogccaaat	actggatgta	catcattccc	gtcgtcctgt	tctcatgat	800
gtcaggagcg	ccagacaccg	ggggccaggg	tgggggtggg	ggtgggggtg	850
gtggtggggg	tagtggcctt	tgctgtgtgc	caccctccct	gtaagtctat	900
ttaaaaacat	cgacgataca	ttgaaatgtg	tgaacgtttt	gaaaagctac	950
agcttccagc	agccaaaagc	aactgttgtt	ttggcaagac	ggtcctgatg	1000
tacaagcttg	attgaaattc	actgctcact	tgatacgtta	ttcagaaacc	1050
caaggaatgg	ctgtcccat	cctcatgtgg	ctgtgtggag	ctcagctgtg	1100
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<210> 372

<211> 269

<212> PRT

<213> Homo sapiens

<400> 372

Met Ala Ala Ala Ser Ala Gly Ala Thr Arg Leu Leu Leu Leu Leu  
1 5 10 15

Leu Met Ala Val Ala Ala Pro Ser Arg Ala Arg Gly Ser Gly Cys  
20 25 30

Arg Ala Gly Thr Gly Ala Arg Gly Ala Gly Ala Glu Gly Arg Glu  
35 40 45

Gly	Glu	Ala	Cys	Gly	Thr	Val	Gly	Leu	Leu	Leu	Glu	His	Ser	Phe	
				50					55					60	
Glu	Ile	Asp	Asp	Ser	Ala	Asn	Phe	Arg	Lys	Arg	Gly	Ser	Leu	Leu	
				65					70					75	
Trp	Asn	Gln	Gln	Asp	Gly	Thr	Leu	Ser	Leu	Ser	Gln	Arg	Gln	Leu	
				80					85					90	
Ser	Glu	Glu	Glu	Arg	Gly	Arg	Leu	Arg	Asp	Val	Ala	Ala	Leu	Asn	
				95					100					105	
Gly	Leu	Tyr	Arg	Val	Arg	Ile	Pro	Arg	Arg	Pro	Gly	Ala	Leu	Asp	
				110					115					120	
Gly	Leu	Glu	Ala	Gly	Gly	Tyr	Val	Ser	Ser	Phe	Val	Pro	Ala	Cys	
				125					130					135	
Ser	Leu	Val	Glu	Ser	His	Leu	Ser	Asp	Gln	Leu	Thr	Leu	His	Val	
				140					145					150	
Asp	Val	Ala	Gly	Asn	Val	Val	Gly	Val	Ser	Val	Val	Thr	His	Pro	
				155					160					165	
Gly	Gly	Cys	Arg	Gly	His	Glu	Val	Glu	Asp	Val	Asp	Leu	Glu	Leu	
				170					175					180	
Phe	Asn	Thr	Ser	Val	Gln	Leu	Gln	Pro	Pro	Thr	Thr	Ala	Pro	Gly	
				185					190					195	
Pro	Glu	Thr	Ala	Ala	Phe	Ile	Glu	Arg	Leu	Glu	Met	Glu	Gln	Ala	
				200					205					210	
Gln	Lys	Ala	Lys	Asn	Pro	Gln	Glu	Gln	Lys	Ser	Phe	Phe	Ala	Lys	
				215					220					225	
Tyr	Trp	Met	Tyr	Ile	Ile	Pro	Val	Val	Leu	Phe	Leu	Met	Met	Ser	
				230					235					240	
Gly	Ala	Pro	Asp	Thr	Gly	Gly	Gln	Gly	Gly	Gly	Gly	Gly	Gly	Gly	
				245					250					255	
Gly	Gly	Gly	Gly	Ser	Gly	Leu	Cys	Cys	Val	Pro	Pro	Ser	Leu		
				260					265						

<210> 373  
 <211> 1706  
 <212> DNA  
 <213> Homo sapiens

<400> 373  
 ggagcgtctgc tggaacccga gccggagccg gagccacagc ggggaggggtg 50  
 gcctggcgcc ctggagcccg acgtgtccgg ggcgtccccg cagaccgggg 100  
 cagcaggtcg tccgggggcc caccatgctg gtgactgcct accttgcttt 150  
 tgtaggcctc ctggcctcct gcctgggggt ggaactgtca agatgccggg 200





**P**

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<210> 374
<211> 450
<212> PRT
<213> Homo sapiens
```

Met   Leu   Val   Thr   Ala   Tyr   Leu   Ala   Phe   Val   Gly   Leu   Leu   Ala   Ser  
1                      5                      10                      15

Arg Ala Cys Ser Asn Pro Ser Phe Leu Arg Phe Gln Leu Asp Phe  
35 40 45

Pro Tyr Leu Tyr Lys Leu Tyr Gln His Tyr Tyr Phe Leu Glu Gly  
65 70 75

Phe Gly Leu Val Ala Ser Ser Leu Val Asp Trp Leu Gly Arg Lys  
95 100 105

Thr Lys Leu Ser Gln Asp Tyr Phe Val Leu Leu Val Gly Arg Ala  
125 130 135

Trp Tyr Ile His Glu His Val Glu Arg His Asp Phe Pro Ala Glu  
155 160 165

Leu Ala Val Val Ala Gly Val Ala Ala Glu Ala Val Ala Ser Trp  
185 190 195

Leu Ala Leu Ala Gly Ala Leu Ala Leu Arg Asn Trp Gly Glu Asn  
215 220 225

Tyr Asp Arg Gln Arg Ala Phe Ser Arg Thr Cys Ala Gly Gly Leu  
230 235 240



ccttggtcccc gctgaacctc cagaggcctg cggggaactc agcaacggtt 300  
 ttttcatcca ggaccagatt gctctggttg agaggggggg ctgctccttc 350  
 ctctccaaga ctggggtggt ccaggagcac ggcgggcggg cggtgatcat 400  
 ctctgacaac gcagttgaca atgacagctt ctacgtggag atgatccagg 450  
 acagtaccca ggcacagct gacatccccg ccctcttctt gctcggccga 500  
 gacggctaca tgatccgccg ctctctggaa cagcatgggc tgccatgggc 550  
 catcatttcc atcccagtca atgtcaccag catccccacc tttagactgc 600  
 tgcaaccgcc ctggaccttc tggtagaaga gtttgtcca cattccagcc 650  
 ataagtgaact ctgagctggg aaggggaaac ccaggaattt tgctacttgg 700  
 aatttgagga tagcatctgg ggacaagtgg agccaggtag aggaaaaggg 750  
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 cccagggccc ccaagggtgt ctcatgttac aagaagaggc aagagacagg 850  
 cccaggggct tctggctaga acccgaaaca aaaggagctg aaggcaggtg 900  
 gcttgagagc catctgtgac ctgtcacact cacctggctc cagcctcccc 950  
 taccaggggt ctctgcacag tgaccttcac agcagttggt ggagtgggtt 1000  
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 taaagcttct catcagggtt gcaaaaaaaaa aaaaaaaaaa aaaaaaaa 1098

<210> 376

<211> 188

<212> PRT

<213> Homo sapiens

<400> 376

Met	Val	Pro	Gly	Ala	Ala	Gly	Trp	Cys	Cys	Leu	Val	Leu	Trp	Leu
1				5					10					15
Pro	Ala	Cys	Val	Ala	Ala	His	Gly	Phe	Arg	Ile	His	Asp	Tyr	Leu
			20						25					30
Tyr	Phe	Gln	Val	Leu	Ser	Pro	Gly	Asp	Ile	Arg	Tyr	Ile	Phe	Thr
			35						40					45
Ala	Thr	Pro	Ala	Lys	Asp	Phe	Gly	Gly	Ile	Phe	His	Thr	Arg	Tyr
			50						55					60
Glu	Gln	Ile	His	Leu	Val	Pro	Ala	Glu	Pro	Pro	Glu	Ala	Cys	Gly
			65						70					75
Glu	Leu	Ser	Asn	Gly	Phe	Phe	Ile	Gln	Asp	Gln	Ile	Ala	Leu	Val
			80						85					90

Glu Arg Gly Gly Cys Ser Phe Leu Ser Lys Thr Arg Val Val Gln  
95 100 105

Glu His Gly Gly Arg Ala Val Ile Ile Ser Asp Asn Ala Val Asp  
110 115 120

Asn Asp Ser Phe Tyr Val Glu Met Ile Gln Asp Ser Thr Gln Arg  
125 130 135

Thr Ala Asp Ile Pro Ala Leu Phe Leu Leu Gly Arg Asp Gly Tyr  
140 145 150

Met Ile Arg Arg Ser Leu Glu Gln His Gly Leu Pro Trp Ala Ile  
155 160 165

Ile Ser Ile Pro Val Asn Val Thr Ser Ile Pro Thr Phe Glu Leu  
170 175 180

Leu Gln Pro Pro Trp Thr Phe Trp  
185

<210> 377  
<211> 496  
<212> DNA  
<213> Artificial

<220>  
<221> unsure  
<222> 396  
<223> unknown base

<400> 377  
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ggctggtggt gatggctggt gtgattccaa tccagggcgg gatcctgaac 100  
ctgaacaaga tgggtcaagca agtgactggg aaaatgcccc toctctccta 150  
ctggccctac ggctgtcact gcggactagg tggcagaggc caacccaaag 200  
atgccacgga ctgggtgctgc cagacccatg actgctgcta tgaccacctg 250  
aagaccacag ggtgcggcat ctacaaggac aacaacaaaa gcagcataca 300  
ttgtatggat ttatctcaac gctattgttt aatggctgtg tttaatgtga 350  
tctatctgga aaatgaggac tccgaataaa aagctattac tawttnaaaa 400  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 450  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 496

<210> 378  
<211> 116  
<212> PRT  
<213> Homo sapiens

<400> 378



<223> Synthetic construct.

<400> 381

ctgaacaaga tggtaagca agtgactggg aaaatgccca tcttc 45

<210> 382

<211> 764

<212> DNA

<213> Homo sapiens

<400> 382

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gccctgggat gcaccggcca gaggccatgc tgctgctgct cacgcttgcc 150

ctcctggggg gcccacctg ggaggggaag atgtatggcc ctggaggagg 200

caagtatttc agcaccactg aagactacga ccatgaaatc acagggtgct 250

gggtgtctgt aggtcttctc ctggtgaaaa gtgtccaggt gaaacttgga 300

gactcctggg acgtgaaact gggagcctta ggtgggaata cccaggaagt 350

caccctgcag ccaggcgaat acatcacaaa agtctttgtc gccttccaag 400

ctttcctccg gggatggtc atgtacacca gcaaggaccg ctatttctat 450

tttgggaagc ttgatggcca gatctcctct gcctaccca gccagagg 500

gcagggtgctg gtgggcatct atggccagta tcaactcctt ggcatcaaga 550

gcattggctt tgaatggaat tatccactag aggagccgac cactgagcca 600

ccagttaatc tcacatactc agcaaactca cccgtgggtc gctaggggtg 650

ggtatggggc catccgagct gaggccatct gtgtgggtgg ggctgatgg 700

actggagtaa ctgagtcggg acgctgaatc tgaatccacc aataaataaa 750

gcttctgcag aaaa 764

<210> 383

<211> 178

<212> PRT

<213> Homo sapiens

<400> 383

Met His Arg Pro Glu Ala Met Leu Leu Leu Leu Thr Leu Ala Leu  
1 5 10 15

Leu Gly Gly Pro Thr Trp Ala Gly Lys Met Tyr Gly Pro Gly Gly  
20 25 30

Gly Lys Tyr Phe Ser Thr Thr Glu Asp Tyr Asp His Glu Ile Thr  
35 40 45

T090227.230001

Gly Leu Arg Val Ser Val Gly Leu Leu Leu Val Lys Ser Val Gln  
50 55 60  
Val Lys Leu Gly Asp Ser Trp Asp Val Lys Leu Gly Ala Leu Gly  
65 70 75  
Gly Asn Thr Gln Glu Val Thr Leu Gln Pro Gly Glu Tyr Ile Thr  
80 85 90  
Lys Val Phe Val Ala Phe Gln Ala Phe Leu Arg Gly Met Val Met  
95 100 105  
Tyr Thr Ser Lys Asp Arg Tyr Phe Tyr Phe Gly Lys Leu Asp Gly  
110 115 120  
Gln Ile Ser Ser Ala Tyr Pro Ser Gln Glu Gly Gln Val Leu Val  
125 130 135  
Gly Ile Tyr Gly Gln Tyr Gln Leu Leu Gly Ile Lys Ser Ile Gly  
140 145 150  
Phe Glu Trp Asn Tyr Pro Leu Glu Glu Pro Thr Thr Glu Pro Pro  
155 160 165  
Val Asn Leu Thr Tyr Ser Ala Asn Ser Pro Val Gly Arg  
170 175

<210> 384  
<211> 2379  
<212> DNA  
<213> Homo sapiens

<400> 384  
gctgagcgtg tgcgcggtac ggggctctcc tgccttctgg gctccaacgc 50  
agctctgtgg ctgaactggg tgctcatcac ggggaactgct gggctatgga 100  
atacagatgt ggcagctcag gtagcccaa attgcctgga agaatacatc 150  
atgtttttcg ataagaagaa attgtaggat ccagtttttt ttttaaccgc 200  
cccctcccca cccccaaaa aaactgtaaa gatgcaaaaa cgtaatatcc 250  
atgaagatcc tattacctag gaagattttg atgttttgct gcgaatgcgg 300  
tgttgggatt tatttgttct tggagtgttc tgcgtggctg gcaaagaata 350  
atgttccaaa atcgggtccat ctcccaaggg gtccaatttt tcttctctggg 400  
tgtcagcgag cctgaactca ctacagtgcg gctgacaggg gctgtcatgc 450  
aactggcccc taagccaaag caaaagacct aaggacgacc tttgaacaat 500  
acaaaggatg ggtttcaatg taattaggct actgagcgga tcagctgtag 550  
cactgggtat agccccact gtcttactga caatgctttc ttctgccgaa 600  
cgaggatgcc ctaagggtg taggtgtgaa ggcaaatgg tatattgtga 650





ttgaactctg gtgactatca agggaaacgcg atgccccccc tccccttccc 2150  
 tctccctctc acttttggtgg caagatcctt ccttgtccgt tttagtgcac 2200  
 tcataatact ggtcattttc ctctcataca taatcaaccc attgaaattt 2250  
 aaataccaca atcaatgtga agcttgaact ccggtttaat ataataccta 2300  
 ttgtataaga ccctttactg attccattaa tgtcgcattt gttttaagat 2350  
 aaaacttctt tcataggtaa aaaaaaaaaa 2379

<210> 385

<211> 513

<212> PRT

<213> Homo sapiens

<400> 385

Met	Gly	Phe	Asn	Val	Ile	Arg	Leu	Leu	Ser	Gly	Ser	Ala	Val	Ala	1	5	10	15
Leu	Val	Ile	Ala	Pro	Thr	Val	Leu	Leu	Thr	Met	Leu	Ser	Ser	Ala	20	25	30	
Glu	Arg	Gly	Cys	Pro	Lys	Gly	Cys	Arg	Cys	Glu	Gly	Lys	Met	Val	35	40	45	
Tyr	Cys	Glu	Ser	Gln	Lys	Leu	Gln	Glu	Ile	Pro	Ser	Ser	Ile	Ser	50	55	60	
Ala	Gly	Cys	Leu	Gly	Leu	Ser	Leu	Arg	Tyr	Asn	Ser	Leu	Gln	Lys	65	70	75	
Leu	Lys	Tyr	Asn	Gln	Phe	Lys	Gly	Leu	Asn	Gln	Leu	Thr	Trp	Leu	80	85	90	
Tyr	Leu	Asp	His	Asn	His	Ile	Ser	Asn	Ile	Asp	Glu	Asn	Ala	Phe	95	100	105	
Asn	Gly	Ile	Arg	Arg	Leu	Lys	Glu	Leu	Ile	Leu	Ser	Ser	Asn	Arg	110	115	120	
Ile	Ser	Tyr	Phe	Leu	Asn	Asn	Thr	Phe	Arg	Pro	Val	Thr	Asn	Leu	125	130	135	
Arg	Asn	Leu	Asp	Leu	Ser	Tyr	Asn	Gln	Leu	His	Ser	Leu	Gly	Ser	140	145	150	
Glu	Gln	Phe	Arg	Gly	Leu	Arg	Lys	Leu	Leu	Ser	Leu	His	Leu	Arg	155	160	165	
Ser	Asn	Ser	Leu	Arg	Thr	Ile	Pro	Val	Arg	Ile	Phe	Gln	Asp	Cys	170	175	180	
Arg	Asn	Leu	Glu	Leu	Leu	Asp	Leu	Gly	Tyr	Asn	Arg	Ile	Arg	Ser	185	190	195	
Leu	Ala	Arg	Asn	Val	Phe	Ala	Gly	Met	Ile	Arg	Leu	Lys	Glu	Leu				

				200					205					210
His	Leu	Glu	His	Asn 215	Gln	Phe	Ser	Lys	Leu 220	Asn	Leu	Ala	Leu	Phe 225
Pro	Arg	Leu	Val	Ser 230	Leu	Gln	Asn	Leu	Tyr 235	Leu	Gln	Trp	Asn	Lys 240
Ile	Ser	Val	Ile	Gly 245	Gln	Thr	Met	Ser	Trp 250	Thr	Trp	Ser	Ser	Leu 255
Gln	Arg	Leu	Asp	Leu 260	Ser	Gly	Asn	Glu	Ile 265	Glu	Ala	Phe	Ser	Gly 270
Pro	Ser	Val	Phe	Gln 275	Cys	Val	Pro	Asn	Leu 280	Gln	Arg	Leu	Asn	Leu 285
Asp	Ser	Asn	Lys	Leu 290	Thr	Phe	Ile	Gly	Gln 295	Glu	Ile	Leu	Asp	Ser 300
Trp	Ile	Ser	Leu	Asn 305	Asp	Ile	Ser	Leu	Ala 310	Gly	Asn	Ile	Trp	Glu 315
Cys	Ser	Arg	Asn	Ile 320	Cys	Ser	Leu	Val	Asn 325	Trp	Leu	Lys	Ser	Phe 330
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Cys	Gly	Lys	Ser	Thr 365	Thr	Glu	Arg	Phe	Asp 370	Leu	Ala	Arg	Ala	Leu 375
Pro	Lys	Pro	Thr	Phe 380	Lys	Pro	Lys	Leu	Pro 385	Arg	Pro	Lys	His	Glu 390
Ser	Lys	Pro	Pro	Leu 395	Pro	Pro	Thr	Val	Gly 400	Ala	Thr	Glu	Pro	Gly 405
Pro	Glu	Thr	Asp	Ala 410	Asp	Ala	Glu	His	Ile 415	Ser	Phe	His	Lys	Ile 420
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Leu	Val	Ile	Tyr	Val 440	Ser	Trp	Lys	Arg	Tyr 445	Pro	Ala	Ser	Met	Lys 450
Gln	Leu	Gln	Gln	Arg 455	Ser	Leu	Met	Arg	Arg 460	His	Arg	Lys	Lys	Lys 465
Arg	Gln	Ser	Leu	Lys 470	Gln	Met	Thr	Pro	Ser 475	Thr	Gln	Glu	Phe	Tyr 480
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Val	Phe	Ala	Val	Gly	Asp	Leu	Asp	Ser	Ile	Tyr	Gly	Thr	Glu	Ala	
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- <222> 1-26
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<212> PRT

<213> Homo sapiens

<400> 395

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Gly Leu Gly Pro His Ile Met Pro Val Pro Ile Pro Leu Asp Thr  
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Ala His Leu Asp Leu Ser Ser Asn Arg Leu Glu Met Val Asn Glu  
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Ser Val Leu Ala Gly Pro Gly Tyr Thr Thr Leu Ala Gly Leu Asp  
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95 100 105  
Arg Leu Arg Tyr Leu Glu Ser Leu Asp Leu Ser His Asn Gly Leu  
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Val Asn Leu Ser His Asn Gln Leu Arg Glu Val Ser Val Ser Ala  
140 145 150





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Gly Ala Thr Thr Cys Ala Thr Asn Ser His Ser Asp Ser Glu Leu  
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<213> Homo sapiens

<400> 406  
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315

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<222> 1-34

<223> Synthetic construct.

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<211> 1487

<212> DNA

<213> Homo sapiens

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cagctacctg	ggaggctgag	gcaggagaat	cgcttgaacc	cggggggcag	1150
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<213> Homo sapiens

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20 25 30

Gly Ile Leu Phe Phe Thr Gly Trp Trp Ile Met Ile Asp Ala Ala  
35 40 45

Val Val Tyr Pro Lys Pro Glu Gln Leu Asn His Ala Phe His Thr  
50 55 60

Cys Gly Val Phe Ser Thr Leu Ala Phe Phe Met Ile Asn Ala Val  
65 70 75

Ser Asn Ala Gln Val Arg Gly Asp Ser Tyr Glu Ser Gly Cys Leu  
80 85 90

Gly Arg Thr Gly Ala Arg Val Trp Leu Phe Ile Gly Phe Met Leu  
95 100 105

Met Phe Gly Ser Leu Ile Ala Ser Met Trp Ile Leu Phe Gly Ala  
110 115 120

Tyr Val Thr Gln Asn Thr Asp Val Tyr Pro Gly Leu Ala Val Phe  
125 130 135

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<210> 414

<211> 1337  
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<400> 414

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actgcatcta gaggagggcc gtctgtgagg ccactacccc tccagcaact 150  
gggaggtggg actgtcagaa gctggcccag ggtggtggtc agctgggtca 200  
gggacctacg gcacctgctg gaccacctcg ccttctccat cgaagcaggg 250  
aagtgggagc ctcgagccct cgggtggaag ctgaccccaa gccacccttc 300  
acctggacag gatgagagtg tcaggtgtgc ttgcctcctt ggcctcctc 350  
tttgccatag tcacgacatg gatgtttatt cgaagctaca tgagcttcag 400  
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 <212> PRT  
 <213> Homo sapiens

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 Met Lys Thr Ile Arg Leu Pro Arg Trp Leu Ala Ala Ser Pro Thr  
 35 40 45  
 Lys Glu Ile Gln Val Lys Lys Tyr Lys Cys Gly Leu Ile Lys Pro  
 50 55 60  
 Cys Pro Ala Asn Tyr Phe Ala Phe Lys Ile Cys Ser Gly Ala Ala  
 65 70 75  
 Asn Val Val Gly Pro Thr Met Cys Phe Glu Asp Arg Met Ile Met  
 80 85 90  
 Ser Pro Val Lys Asn Asn Val Gly Arg Gly Leu Asn Ile Ala Leu  
 95 100 105  
 Val Asn Gly Thr Thr Gly Ala Val Leu Gly Gln Lys Ala Phe Asp  
 110 115 120  
 Met Tyr Ser Gly Asp Val Met His Leu Val Lys Phe Leu Lys Glu  
 125 130 135  
 Ile Pro Gly Gly Ala Leu Val Leu Val Ala Ser Tyr Asp Asp Pro  
 140 145 150  
 Gly Thr Lys Met Asn Asp Glu Ser Arg Lys Leu Phe Ser Asp Leu  
 155 160 165  
 Gly Ser Ser Tyr Ala Lys Gln Leu Gly Phe Arg Asp Ser Trp Val  
 170 175 180  
 Phe Ile Gly Ala Lys Asp Leu Arg Gly Lys Ser Pro Phe Glu Gln  
 185 190 195  
 Phe Leu Lys Asn Ser Pro Asp Thr Asn Lys Tyr Glu Gly Trp Pro  
 200 205 210  
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 215 220

<210> 416  
 <211> 21  
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<220>  
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<222> 1-21  
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 <220>  
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 <222> 1-18  
 <223> Synthetic construct.  
  
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 <210> 418  
 <211> 26  
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 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-26  
 <223> Synthetic construct.  
  
 <400> 418  
 aaagtacaag tgtggcctca tcaagc 26  
  
 <210> 419  
 <211> 24  
 <212> DNA  
 <213> Artificial  
  
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 <222> 1-24  
 <223> Synthetic construct.  
  
 <400> 419  
 tctgactcct aagtcaggca ggag 24  
  
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 <211> 24  
 <212> DNA  
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 <220>  
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 <222> 1-24  
 <223> Synthetic construct.  
  
 <400> 420  
 attctctcca cagacagctg gttc 24

<210> 421  
<211> 46  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-46  
<223> Synthetic construct.

<400> 421  
gtacaagtgt ggccatcatca agccctgccc agccaactac tttgcg 46

<210> 422  
<211> 1701  
<212> DNA  
<213> Homo sapiens

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<400> 422  
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tggaagccca cagagacaga gacagcaaga gaagcagaga taaatacact 150  
cacgccagga gctcgctcgc tctctctctc tctctctcac tcttccctcc 200  
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acatgggtcag gaccattggc cagcctctta ccctgagtgt ggaaacaatg 400  
cccagtcgcc catcgatatt cagacagaca gtgtgacatt tgaccctgat 450  
ttgcctgctc tgcagcccca cggatatgac cagcctggca ccgagccttt 500  
ggacctgcac aacaatggcc acacagtgca actctctctg ccctctaccc 550  
tgtatctggg tggacttccc cgaaaatatg tagctgcca gctccacctg 600  
cactgggggtc agaaaggatc ccaggggggg tcagaacacc agatcaacag 650  
tgaagccaca tttgcagagc tccacattgt acattatgac tctgattcct 700  
atgacagctt gagtgaggct gctgagaggc ctcagggcct ggctgtcctg 750  
ggcatcctaa ttgaggtggg tgagactaag aatatagctt atgaacacat 800  
tctgagtcac ttgcatgaag tcaggcataa agatcagaag acctcagtgc 850





80									85					90	
Pro	Ser	Thr	Leu	Tyr 95	Leu	Gly	Gly	Leu	Pro 100	Arg	Lys	Tyr	Val	Ala 105	
Ala	Gln	Leu	His	Leu 110	His	Trp	Gly	Gln	Lys 115	Gly	Ser	Pro	Gly	Gly 120	
Ser	Glu	His	Gln	Ile 125	Asn	Ser	Glu	Ala	Thr 130	Phe	Ala	Glu	Leu	His 135	
Ile	Val	His	Tyr	Asp 140	Ser	Asp	Ser	Tyr	Asp 145	Ser	Leu	Ser	Glu	Ala 150	
Ala	Glu	Arg	Pro	Gln 155	Gly	Leu	Ala	Val	Leu 160	Gly	Ile	Leu	Ile	Glu 165	
Val	Gly	Glu	Thr	Lys 170	Asn	Ile	Ala	Tyr	Glu 175	His	Ile	Leu	Ser	His 180	
Leu	His	Glu	Val	Arg 185	His	Lys	Asp	Gln	Lys 190	Thr	Ser	Val	Pro	Pro 195	
Phe	Asn	Leu	Arg	Glu 200	Leu	Leu	Pro	Lys	Gln 205	Leu	Gly	Gln	Tyr	Phe 210	
Arg	Tyr	Asn	Gly	Ser 215	Leu	Thr	Thr	Pro	Pro 220	Cys	Tyr	Gln	Ser	Val 225	
Leu	Trp	Thr	Val	Phe 230	Tyr	Arg	Arg	Ser	Gln 235	Ile	Ser	Met	Glu	Gln 240	
Leu	Glu	Lys	Leu	Gln 245	Gly	Thr	Leu	Phe	Ser 250	Thr	Glu	Glu	Glu	Pro 255	
Ser	Lys	Leu	Leu	Val 260	Gln	Asn	Tyr	Arg	Ala 265	Leu	Gln	Pro	Leu	Asn 270	
Gln	Arg	Met	Val	Phe 275	Ala	Ser	Phe	Ile	Gln 280	Ala	Gly	Ser	Ser	Tyr 285	
Thr	Thr	Gly	Glu	Met 290	Leu	Ser	Leu	Gly	Val 295	Gly	Ile	Leu	Val	Gly 300	
Cys	Leu	Cys	Leu	Leu 305	Leu	Ala	Val	Tyr	Phe 310	Ile	Ala	Arg	Lys	Ile 315	
Arg	Lys	Lys	Arg	Leu 320	Glu	Asn	Arg	Lys	Ser 325	Val	Val	Phe	Thr	Ser 330	
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<211> 18
<212> DNA
<213> Artificial
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<220>  
 <221> Artificial Sequence  
 <222> 1-18  
 <223> Synthetic construct.

<400> 424  
 gtaaagtcgc tggccagc 18

<210> 425  
 <211> 18  
 <212> DNA  
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<220>  
 <221> Artificial Sequence  
 <222> 1-18  
 <223> Synthetic construct.

<400> 425  
 cccgatctgc ctgctgta 18

<210> 426  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 426  
 ctgcactgta tggccattat tgtg 24

<210> 427  
 <211> 45  
 <212> DNA  
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<220>  
 <221> Artificial Sequence  
 <222> 1-45  
 <223> Synthetic construct.

<400> 427  
 cagaaaccca tgatacccta ctgaacaccg aatccccctgg aagcc 45

<210> 428  
 <211> 1073  
 <212> DNA  
 <213> Homo sapiens

<400> 428  
 aatttttcac cagagtaaac ttgagaaacc aactggacct tgagtattgt 50  
 acattttgcc tcgtggaccc aaaggtagca atctgaaaca tgaggagtac 100  
 gattctactg ttttgtcttc taggatcaac tcggtcatta ccacagctca 150

aacctgcttt	gggactccct	cccacaaaac	tggctccgga	tcagggaaca	200
ctaccaaacc	aacagcagtc	aaatcaggtc	tttccttctt	taagtctgat	250
accattaaca	cagatgctca	cactgggggc	agatctgcat	ctgttaaadc	300
ctgctgcagg	aatgacacct	ggtaccaga	cccaccatt	gacctggga	350
gggttgaatg	tacaacagca	actgcacca	catgtgttac	caatttttgt	400
cacacaactt	ggagcccagg	gcactatcct	aagctcagag	gaattgccac	450
aaatcttcac	gagcctcatc	atccattcct	tgttcccgga	aggcatcctg	500
cccaccagtc	aggcaggggc	taatccagat	gtccaggatg	gaagccttcc	550
agcaggagga	gcagggtgaa	atcctgccac	ccagggaacc	ccagcaggcc	600
gcctcccaac	tcccagtggc	acagatgacg	actttgcagt	gaccaccctt	650
gcaggcatcc	aaaggagcac	acatgccatc	gaggaagcca	ccacagaatc	700
agcaaatgga	attcagtaag	ctgtttcaaa	ttttttcaac	taagctgcct	750
cgaatttggt	gatacatgtg	aatctttatc	attgattata	ttatggaata	800
gattgagaca	cattggatag	tcttagaaga	aattaattct	taatttacct	850
gaaaatattc	ttgaaatttc	agaaaatatg	ttctatgtag	agaatcccaa	900
cttttaaaaa	caataattca	atggataaat	ctgtctttga	aatataacat	950
tatgctgcct	ggatgatatg	catattaaaa	catatttgga	aaactggaaa	1000
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<212> PRT
<213> Homo sapiens
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Ser Leu Pro Gln Leu Lys Pro Ala Leu Gly Leu Pro Pro Thr Lys
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Leu Ala Pro Asp Gln Gly Thr Leu Pro Asn Gln Gln Gln Ser Asn
             35             40             45

Gln Val Phe Pro Ser Leu Ser Leu Ile Pro Leu Thr Gln Met Leu
             50             55             60

Thr Leu Gly Pro Asp Leu His Leu Leu Asn Pro Ala Ala Gly Met
             65             70             75

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Ala Leu Arg Val Leu Phe Ser Gly Ser Leu Arg Leu Lys Cys Arg  
140 145 150

Asn Ala Cys Cys Gln Arg Trp Tyr Phe Thr Phe Asn Gly Ala Glu  
155 160 165

Cys Ser Gly Pro Leu Pro Ile Glu Ala Ile Ile Tyr Leu Asp Gln  
170 175 180

Gly Ser Pro Glu Met Asn Ser Thr Ile Asn Ile His Arg Thr Ser  
185 190 195

Ser Val Glu Gly Leu Cys Glu Gly Ile Gly Ala Gly Leu Val Asp  
200 205 210

Val Ala Ile Trp Val Gly Thr Cys Ser Asp Tyr Pro Lys Gly Asp  
215 220 225

Ala Ser Thr Gly Trp Asn Ser Val Ser Arg Ile Ile Ile Glu Glu  
230 235 240

Leu Pro Lys

<210> 432

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificial Sequence

<400> 432

aggacttgcc ctcaggaa 18

<210> 433

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 433

cgcaggacag ttgtgaaaat a 21

<210> 434

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 434

atgacgctcg tccaaggcca c 21

<210> 435

<211> 19  
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 cccacctgta ccaccatgt 19  
  
 <210> 436  
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 <223> Synthetic oligonucleotide probe  
  
 <400> 436  
 actccaggca ccatctgttc tccc 24  
  
 <210> 437  
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 aagggctggc attcaagtc 19  
  
 <210> 438  
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 tgacctggca aaggaagaa 19  
  
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 cagccaccct ccagtccaag g 21  
  
 <210> 440  
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<220>  
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<400> 440  
gggtcgtggt ttggagaga 19

<210> 441  
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ctggccctca gagcaccaat 20

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<210> 443  
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<400> 443  
ctggcaggag ttaaagttcc aaga 24

<210> 444  
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<400> 444  
aaaggacacc gggatgtg 18

<210> 445  
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<400> 445  
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 <210> 447  
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 caggactgag cgcttggtta 20  
  
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 caaagcgcca agtaccggac c 21  
  
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 ccagacctca gccaggaa 18  
  
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 ccctagctga ccccttca 18

<210> 451  
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<212> DNA  
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<220>  
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<400> 451  
tctgacaagc agttttctga atc 23

<210> 452  
<211> 26  
<212> DNA  
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<220>  
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<400> 452  
ctctccccct cccttttcct ttgttt 26

<210> 453  
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<220>  
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<210> 455  
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<210> 456  
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<220>

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<400> 456

ccttgaaaag gaccagttt 20

<210> 457

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 457

atgagtcgca cctgctgttc cc 22

<210> 458

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 458

tagcagctgc ccttggtta 18

<210> 459

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 459

aacagcaggt gcgactcatc ta 22

<210> 460

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 460

tgctaggcga cgacacccag acc 23

<210> 461

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 461

tggacacgtg gcagtgga 18

<210> 462

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 462

tcatggtctc gtccattc 19

<210> 463

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 463

caccatttgt ttctctgtct ccccatc 27

<210> 464

<211> 18

<212> DNA

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<220>

<223> Synthetic oligonucleotide probe

<400> 464

ccggcatcct tggagtag 18

<210> 465

<211> 20

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<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 465

tccccattag cacaggagta 20

<210> 466

<211> 23

<212> DNA

<213> Artificial Sequence

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<400> 466

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<213> Artificial Sequence

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actgctccgc ctactacga 19

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aggcatcctc gccgtcctca 20

<213> Artificial Sequence

<223> Synthetic oligonucleotide probe

aaggccaagg tgagtccat 19

<213> Artificial Sequence

<223> Synthetic oligonucleotide probe

cgagtgtgtg cgaaacctaa 20

<210> 472

<211> 24  
<212> DNA  
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<220>  
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<400> 472  
tcagggtcta catcagcctc ctgc 24

<210> 473  
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<400> 473  
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<210> 474  
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